

SEQUENCE LISTING

<110> Xiao-Qing Qiu

<120> METHODS AND COMPOSITIONS FOR THE
TREATMENT OF INFECTION

<130> JSI-002

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 633

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDI

<400> 1

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Ser Asp Pro Val Arg Ile Thr Asn Pro Gly Ala Glu Ser Leu Gly Tyr
 1           5           10          15
Asp Ser Asp Gly His Glu Ile Met Ala Val Asp Ile Tyr Val Asn Pro
 20          25          30
Pro Arg Val Asp Val Phe His Gly Thr Pro Pro Ala Trp Ser Ser Phe
 35          40          45
Gly Asn Lys Thr Ile Trp Gly Gly Asn Glu Trp Val Asp Asp Ser Pro
 50          55          60
Thr Arg Ser Asp Ile Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys
 65          70          75          80
Asn Thr Leu Ser Ala Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu
 85          90          95
Ala Gly Lys Arg Leu Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu
100         105         110
Asn Thr Leu Lys Thr Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile
115         120         125
Thr Arg Gln Glu Phe Arg Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly
130         135         140
Phe Arg Thr Glu Ile Ala Gly Tyr Asp Ala Leu Arg Leu His Thr Glu
145         150         155         160
Ser Arg Met Leu Phe Ala Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg
165         170         175
Glu Ala Arg Ser Leu Ile Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala
180         185         190
Gln Asn Ala Asp Lys Lys Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg
195         200         205
Arg Lys Gly Ile Leu Asp Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly
210         215         220
Gly Ala Ala Leu Ala Val Leu Asp Ala Gln Gln Ala Arg Leu Leu Gly
225         230         235         240
Gln Gln Thr Arg Asn Asp Arg Ala Ile Ser Glu Ala Arg Asn Lys Leu
245         250         255
Ser Ser Val Thr Glu Ser Leu Asn Thr Ala Arg Asn Ala Leu Thr Arg
260         265         270
Ala Glu Gln Gln Leu Thr Gln Gln Lys Asn Thr Pro Asp Gly Lys Thr
275         280         285
Ile Val Ser Pro Glu Lys Phe Pro Gly Arg Ser Ser Thr Asn His Ser

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290		295		300
Ile Val Val Ser Gly Asp	Pro Arg Phe Ala Gly	Thr Ile Lys Ile Thr		
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Thr Ser Ala Val Ile Asp	Asn Arg Ala Asn Leu	Asn Tyr Leu Leu Ser		
	325	330	335	
His Ser Gly Leu Asp Tyr Lys Arg	Asn Ile Leu Asn Asp	Arg Asn Pro		
	340	345	350	
Val Val Thr Glu Asp Val Glu Gly	Asp Lys Lys Ile Tyr	Asn Ala Glu		
	355	360	365	
Val Ala Glu Trp Asp Lys Leu Arg	Gln Arg Leu Leu Asp	Ala Arg Asn		
	370	375	380	
Lys Ile Thr Ser Ala Glu Ser Ala	Val Asn Ser Ala Arg	Asn Asn Leu		
385	390	395	400	
Ser Ala Arg Thr Asn Glu Gln Lys	His Ala Asn Asp	Ala Leu Asn Ala		
	405	410	415	
Leu Leu Lys Glu Lys Glu Asn Ile	Arg Asn Gln Leu Ser	Gly Ile Asn		
	420	425	430	
Gln Lys Ile Ala Glu Glu Lys Arg	Lys Gln Asp Glu Leu	Lys Ala Thr		
	435	440	445	
Lys Asp Ala Ile Asn Phe Thr Thr	Glu Phe Leu Lys	Ser Val Ser Glu		
	450	455	460	
Lys Tyr Gly Ala Lys Ala Glu Gln	Leu Ala Arg Glu	Met Ala Gly Gln		
465	470	475	480	
Ala Lys Gly Lys Lys Ile Arg Asn	Val Glu Glu Ala Leu	Lys Thr Tyr		
	485	490	495	
Glu Lys Tyr Arg Ala Asp Ile Asn	Lys Lys Ile Asn Ala	Lys Asp Arg		
	500	505	510	
Ala Ala Ile Ala Ala Ala Leu Glu	Ser Val Lys Leu Ser	Asp Ile Ser		
	515	520	525	
Ser Asn Leu Asn Arg Phe Ser Arg	Gly Leu Gly Tyr Ala	Gly Lys Phe		
	530	535	540	
Thr Ser Leu Ala Asp Trp Ile Thr	Glu Phe Gly Lys Ala	Val Arg Thr		
545	550	555	560	
Glu Asn Trp Arg Pro Leu Phe Val	Lys Thr Glu Thr Ile	Ile Ala Gly		
	565	570	575	
Asn Ala Ala Thr Ala Leu Val Ala	Leu Val Phe Ser Ile	Leu Thr Gly		
	580	585	590	
Ser Ala Leu Gly Ile Ile Gly Tyr	Gly Leu Leu Met Ala	Val Thr Gly		
	595	600	605	
Ala Leu Ile Asp Glu Ser Leu Val	Glu Lys Ala Asn Lys	Phe Trp Gly		
	610	615	620	
Ile Tyr Ser Thr Cys Asp Phe Ile	Met			
625	630			

<210> 2

<211> 1905

<212> DNA

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDI

<400> 2

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gttgatgatt cccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtactga agccggaaaa 300
cgcctctctg cggcgattgc tgcaagggaa aaagatgaaa acacactgaa aacactccgt 360

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gagagccgga tgctgtttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540
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gctgatatgc ttgctgaata cgagcgcaga aaaggatttc tggacacccg gttgtcagag 660
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tcaacaaatc attctattgt tgtgagcggg gatccgagat ttgccggtac gataaaaaatc 960
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<210> 3

<211> 634

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDII

<400> 3

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Ser Asp Pro Val Arg Ile Thr Asn Pro Gly Ala Glu Ser Leu Gly Tyr
 1           5           10          15
Asp Ser Asp Gly His Glu Ile Met Ala Val Asp Ile Tyr Val Asn Pro
 20          25          30
Pro Arg Val Asp Val Phe His Gly Thr Pro Pro Ala Trp Ser Ser Phe
 35          40          45
Gly Asn Lys Thr Ile Trp Gly Gly Asn Glu Trp Val Asp Asp Ser Pro
 50          55          60
Thr Arg Ser Asp Ile Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys
 65          70          75          80
Asn Thr Leu Ser Ala Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu
 85          90          95
Ala Gly Lys Arg Leu Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu
100          105          110
Asn Thr Leu Lys Thr Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile
115          120          125
Thr Arg Gln Glu Phe Arg Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly
130          135          140
Phe Arg Thr Glu Ile Ala Gly Tyr Asp Ala Leu Arg Leu His Thr Glu
145          150          155          160
Ser Arg Met Leu Phe Ala Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg
165          170          175
Glu Ala Arg Ser Leu Ile Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala
180          185          190

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Gln	Asn	Ala	Asp	Lys	Lys	Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg
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Arg	Lys	Gly	Ile	Leu	Asp	Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly
	210					215					220				
Gly	Ala	Ala	Leu	Ala	Val	Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly
225					230					235					240
Gln	Gln	Thr	Arg	Asn	Asp	Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu
				245					250					255	
Ser	Ser	Val	Thr	Glu	Ser	Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg
		260						265					270		
Ala	Glu	Gln	Gln	Leu	Thr	Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr
		275					280					285			
Ile	Val	Ser	Pro	Glu	Lys	Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser
	290					295					300				
Ile	Val	Val	Ser	Gly	Asp	Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr
305					310					315					320
Thr	Ser	Ala	Val	Ile	Asp	Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser
				325					330					335	
His	Ser	Gly	Leu	Asp	Tyr	Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro
		340						345					350		
Val	Val	Thr	Glu	Asp	Val	Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu
		355					360					365			
Val	Ala	Glu	Trp	Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn
	370					375				380					
Lys	Ile	Thr	Ser	Ala	Glu	Ser	Ala	Val	Asn	Ser	Ala	Arg	Asn	Asn	Leu
385					390					395					400
Ser	Ala	Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala
				405					410					415	
Leu	Leu	Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn
			420					425					430		
Gln	Lys	Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr
		435					440					445			
Lys	Asp	Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu
	450					455				460					
Lys	Tyr	Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln
465					470					475					480
Ala	Lys	Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr
				485					490					495	
Glu	Lys	Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg
			500					505					510		
Ala	Ala	Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser
		515					520					525			
Ser	Asn	Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe
	530					535					540				
Thr	Ser	Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Arg	Thr
545					550					555					560
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly
				565					570					575	
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Val	Phe	Ser	Ile	Leu	Thr	Gly
			580				585						590		
Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala	Val	Thr	Gly
	595					600						605			
Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys	Phe	Trp	Gly
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Ile	Gly	Val	Asn	Ala	Cys	Ser	Ser	Leu	Phe						
625					630										

<210> 4

<211> 1908

<212> DNA

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDII

<400> 4

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gttgatgatt ccccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
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tatggtttac tgatggctgt caccggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattgg agttaacgca tgttcttccc tgtttttaa 1908

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<210> 5

<211> 633

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDIII

<400> 5

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Ser Asp Pro Val Arg Ile Thr Asn Pro Gly Ala Glu Ser Leu Gly Tyr
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Asp Ser Asp Gly His Glu Ile Met Ala Val Asp Ile Tyr Val Asn Pro
 20          25          30
Pro Arg Val Asp Val Phe His Gly Thr Pro Pro Ala Trp Ser Ser Phe
 35          40          45
Gly Asn Lys Thr Ile Trp Gly Gly Asn Glu Trp Val Asp Asp Ser Pro
 50          55          60
Thr Arg Ser Asp Ile Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys
 65          70          75          80

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Asn	Thr	Leu	Ser	Ala	Gln	Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	
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Ala	Gly	Lys	Arg	Leu	Ser	Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	
			100					105					110			
Asn	Thr	Leu	Lys	Thr	Leu	Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	
			115				120					125				
Thr	Arg	Gln	Glu	Phe	Arg	Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	
			130			135					140					
Phe	Arg	Thr	Glu	Ile	Ala	Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	
145				150						155					160	
Ser	Arg	Met	Leu	Phe	Ala	Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	
				165					170					175		
Glu	Ala	Arg	Ser	Leu	Ile	Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	
			180					185					190			
Gln	Asn	Ala	Asp	Lys	Lys	Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	
			195				200					205				
Arg	Lys	Gly	Ile	Leu	Asp	Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	
			210			215					220					
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225					230					235					240	
Gln	Gln	Thr	Arg	Asn	Asp	Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	
				245					250					255		
Ser	Ser	Val	Thr	Glu	Ser	Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	
			260					265					270			
Ala	Glu	Gln	Gln	Leu	Thr	Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	
			275				280					285				
Ile	Val	Ser	Pro	Glu	Lys	Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	
			290			295					300					
Ile	Val	Val	Ser	Gly	Asp	Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	
305				310						315					320	
Thr	Ser	Ala	Val	Ile	Asp	Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	
				325				330						335		
His	Ser	Gly	Leu	Asp	Tyr	Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	
			340					345					350			
Val	Val	Thr	Glu	Asp	Val	Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	
			355				360					365				
Val	Ala	Glu	Trp	Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	
			370			375					380					
Lys	Ile	Thr	Ser	Ala	Glu	Ser	Ala	Val	Asn	Ser	Ala	Arg	Asn	Asn	Leu	
385					390					395					400	
Ser	Ala	Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	
				405					410					415		
Leu	Leu	Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	
			420					425					430			
Gln	Lys	Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	
			435				440					445				
Lys	Asp	Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	
					455						460					
Lys	Tyr	Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	
465					470					475					480	
Ala	Lys	Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	
				485					490					495		
Glu	Lys	Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	
			500					505					510			
Ala	Ala	Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	
			515				520					525				
Ser	Asn	Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	
			530			535					540					
Thr	Ser	Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Arg	Thr	
545					550					555					560	
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly	

	565		570		575										
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Val	Phe	Ser	Ile	Leu	Thr	Gly
	580				585								590		
Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala	Val	Thr	Gly
	595				600								605		
Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys	Phe	Trp	Gly
	610				615							620			
Ile	Tyr	Ile	Asn	Cys	Asp	Phe	Leu	Leu							
625					630										

<210> 6

<211> 1905

<212> DNA

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDIII

<400> 6

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ggtaccccg	ctgcatggag	ttccttcggg	aacaaaacca	tctggggcgg	aaacgagtgg	180
ggtgatgatt	ccccaacccg	aagtgatatc	gaaaaaagg	acaaggaaat	cacagcgtac	240
aaaaacacgc	tcagcgcgca	gcagaaagag	aatgagaata	agcgtactga	agccggaaaa	300
cgctctctcg	cggcgattgc	tgcaagggaa	aaagatgaaa	acacactgaa	aacactccgt	360
gccggaaaacg	cagatgccgc	tgatattaca	cgacaggagt	tcagactcct	gcaggcagag	420
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gctgatatgc	ttgctgaata	cgagcgcaga	aaagggtattc	tggacacccg	gttgtcagag	660
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gggcagcaga	cacggaatga	cagggccatt	tcagaggccc	ggaataaact	cagttcagtg	780
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tcaacaaatc	attctattgt	tgtagcgggt	gatccgagat	ttgccggtag	gataaaaaatc	960
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tatggtttac	tgatggctgt	caccggtgcg	ctgattgatg	aatcgcttgt	ggaaaaagcg	1860
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<210> 7

<211> 633

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding

Staphylococcus aureus AgrDIV

<400> 7

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 20          25          30
Pro Arg Val Asp Val Phe His Gly Thr Pro Pro Ala Trp Ser Ser Phe
 35          40          45
Gly Asn Lys Thr Ile Trp Gly Gly Asn Glu Trp Val Asp Asp Ser Pro
 50          55          60
Thr Arg Ser Asp Ile Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys
 65          70          75          80
Asn Thr Leu Ser Ala Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu
 85          90          95
Ala Gly Lys Arg Leu Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu
100          105          110
Asn Thr Leu Lys Thr Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile
115          120          125
Thr Arg Gln Glu Phe Arg Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly
130          135          140
Phe Arg Thr Glu Ile Ala Gly Tyr Asp Ala Leu Arg Leu His Thr Glu
145          150          155          160
Ser Arg Met Leu Phe Ala Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg
165          170          175
Glu Ala Arg Ser Leu Ile Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala
180          185          190
Gln Asn Ala Asp Lys Lys Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg
195          200          205
Arg Lys Gly Ile Leu Asp Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly
210          215          220
Gly Ala Ala Leu Ala Val Leu Asp Ala Gln Gln Ala Arg Leu Leu Gly
225          230          235          240
Gln Gln Thr Arg Asn Asp Arg Ala Ile Ser Glu Ala Arg Asn Lys Leu
245          250          255
Ser Ser Val Thr Glu Ser Leu Asn Thr Ala Arg Asn Ala Leu Thr Arg
260          265          270
Ala Glu Gln Gln Leu Thr Gln Gln Lys Asn Thr Pro Asp Gly Lys Thr
275          280          285
Ile Val Ser Pro Glu Lys Phe Pro Gly Arg Ser Ser Thr Asn His Ser
290          295          300
Ile Val Val Ser Gly Asp Pro Arg Phe Ala Gly Thr Ile Lys Ile Thr
305          310          315          320
Thr Ser Ala Val Ile Asp Asn Arg Ala Asn Leu Asn Tyr Leu Leu Ser
325          330          335
His Ser Gly Leu Asp Tyr Lys Arg Asn Ile Leu Asn Asp Arg Asn Pro
340          345          350
Val Val Thr Glu Asp Val Glu Gly Asp Lys Lys Ile Tyr Asn Ala Glu
355          360          365
Val Ala Glu Trp Asp Lys Leu Arg Gln Arg Leu Leu Asp Ala Arg Asn
370          375          380
Lys Ile Thr Ser Ala Glu Ser Ala Val Asn Ser Ala Arg Asn Asn Leu
385          390          395          400
Ser Ala Arg Thr Asn Glu Gln Lys His Ala Asn Asp Ala Leu Asn Ala
405          410          415
Leu Leu Lys Glu Lys Glu Asn Ile Arg Asn Gln Leu Ser Gly Ile Asn
420          425          430
Gln Lys Ile Ala Glu Glu Lys Arg Lys Gln Asp Glu Leu Lys Ala Thr
435          440          445
Lys Asp Ala Ile Asn Phe Thr Thr Glu Phe Leu Lys Ser Val Ser Glu
450          455          460

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Lys Tyr Gly Ala Lys Ala Glu Gln Leu Ala Arg Glu Met Ala Gly Gln
465                               470                               475                               480
Ala Lys Gly Lys Lys Ile Arg Asn Val Glu Glu Ala Leu Lys Thr Tyr
                               485                               490                               495
Glu Lys Tyr Arg Ala Asp Ile Asn Lys Lys Ile Asn Ala Lys Asp Arg
                               500                               505                               510
Ala Ala Ile Ala Ala Ala Leu Glu Ser Val Lys Leu Ser Asp Ile Ser
                               515                               520                               525
Ser Asn Leu Asn Arg Phe Ser Arg Gly Leu Gly Tyr Ala Gly Lys Phe
                               530                               535                               540
Thr Ser Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Arg Thr
545                               550                               555                               560
Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala Gly
                               565                               570                               575
Asn Ala Ala Thr Ala Leu Val Ala Leu Val Phe Ser Ile Leu Thr Gly
                               580                               585                               590
Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala Val Thr Gly
                               595                               600                               605
Ala Leu Ile Asp Glu Ser Leu Val Glu Lys Ala Asn Lys Phe Trp Gly
610                               615                               620
Ile Tyr Ser Thr Cys Tyr Phe Ile Met
625                               630

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<210> 8

<211> 1905

<212> DNA

<213> Artificial sequence

<220>

<223> Colicin attached to Pheromone peptide encoding
Staphylococcus aureus AgrDIV

<400> 8

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ggtaccccgc ctgcatggag ttccttcggg aacaaaacca tctggggcgg aaacgagtgg 180
gttgatgatt cccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtaactga agccggaaaa 300
cgctctctcg cggcgattgc tgcaagggaa aaagatgaaa acacactgaa aacactccgt 360
gccggaaacg cagatgccgc tgatattaca cgacaggagt tcagactcct gcaggcagag 420
ctgagagaat acggattccg tactgaaatc gccggatatg acgccctccg gctgcataca 480
gagagccgga tgctgtttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540
tcgttaatcg aacaggctga aaaacggcag aaggatgcgc agaacgcaga caagaaggcc 600
gctgatatgc ttgctgaata cgagcgcaga aaaggatttc tggacacccg gttgtcagag 660
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ctcagtgccg gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcataatc agaagatagc ggaagagaaa 1320
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cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgcagccctt 1560
gagtcgtgta agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620

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tatggttttac tgatggctgt caccgggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattta ttccacctgt tactttataa tgtaa 1905
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<210> 9

<211> 633

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin Ia attached to Pheromone peptide from
Staphylococcus epidermidis

<400> 9

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Ser Asp Pro Val Arg Ile Thr Asn Pro Gly Ala Glu Ser Leu Gly Tyr
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Asp Ser Asp Gly His Glu Ile Met Ala Val Asp Ile Tyr Val Asn Pro
20     25     30
Pro Arg Val Asp Val Phe His Gly Thr Pro Pro Ala Trp Ser Ser Phe
35     40     45
Gly Asn Lys Thr Ile Trp Gly Gly Asn Glu Trp Val Asp Asp Ser Pro
50     55     60
Thr Arg Ser Asp Ile Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys
65     70     75     80
Asn Thr Leu Ser Ala Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu
85     90     95
Ala Gly Lys Arg Leu Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu
100    105    110
Asn Thr Leu Lys Thr Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile
115    120    125
Thr Arg Gln Glu Phe Arg Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly
130    135    140
Phe Arg Thr Glu Ile Ala Gly Tyr Asp Ala Leu Arg Leu His Thr Glu
145    150    155    160
Ser Arg Met Leu Phe Ala Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg
165    170    175
Glu Ala Arg Ser Leu Ile Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala
180    185    190
Gln Asn Ala Asp Lys Lys Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg
195    200    205
Arg Lys Gly Ile Leu Asp Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly
210    215    220
Gly Ala Ala Leu Ala Val Leu Asp Ala Gln Gln Ala Arg Leu Leu Gly
225    230    235    240
Gln Gln Thr Arg Asn Asp Arg Ala Ile Ser Glu Ala Arg Asn Lys Leu
245    250    255
Ser Ser Val Thr Glu Ser Leu Asn Thr Ala Arg Asn Ala Leu Thr Arg
260    265    270
Ala Glu Gln Gln Leu Thr Gln Gln Lys Asn Thr Pro Asp Gly Lys Thr
275    280    285
Ile Val Ser Pro Glu Lys Phe Pro Gly Arg Ser Ser Thr Asn His Ser
290    295    300
Ile Val Val Ser Gly Asp Pro Arg Phe Ala Gly Thr Ile Lys Ile Thr
305    310    315    320
Thr Ser Ala Val Ile Asp Asn Arg Ala Asn Leu Asn Tyr Leu Leu Ser
325    330    335
His Ser Gly Leu Asp Tyr Lys Arg Asn Ile Leu Asn Asp Arg Asn Pro
340    345    350
Val Val Thr Glu Asp Val Glu Gly Asp Lys Lys Ile Tyr Asn Ala Glu
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Val Ala Glu Trp Asp Lys Leu Arg Gln Arg Leu Leu Asp Ala Arg Asn		
370	375	380
Lys Ile Thr Ser Ala Glu Ser Ala Val Asn Ser Ala Arg Asn Asn Leu		
385	390	395
Ser Ala Arg Thr Asn Glu Gln Lys His Ala Asn Asp Ala Leu Asn Ala		400
	405	410
Leu Leu Lys Glu Lys Glu Asn Ile Arg Asn Gln Leu Ser Gly Ile Asn		415
	420	425
Gln Lys Ile Ala Glu Glu Lys Arg Lys Gln Asp Glu Leu Lys Ala Thr		430
	435	440
Lys Asp Ala Ile Asn Phe Thr Thr Glu Phe Leu Lys Ser Val Ser Glu		445
	450	455
Lys Tyr Gly Ala Lys Ala Glu Gln Leu Ala Arg Glu Met Ala Gly Gln		460
465	470	475
Ala Lys Gly Lys Lys Ile Arg Asn Val Glu Glu Ala Leu Lys Thr Tyr		480
	485	490
Glu Lys Tyr Arg Ala Asp Ile Asn Lys Lys Ile Asn Ala Lys Asp Arg		495
	500	505
Ala Ala Ile Ala Ala Ala Leu Glu Ser Val Lys Leu Ser Asp Ile Ser		510
	515	520
Ser Asn Leu Asn Arg Phe Ser Arg Gly Leu Gly Tyr Ala Gly Lys Phe		525
	530	535
Thr Ser Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Arg Thr		540
545	550	555
Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala Gly		560
	565	570
Asn Ala Ala Thr Ala Leu Val Ala Leu Val Phe Ser Ile Leu Thr Gly		575
	580	585
Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala Val Thr Gly		590
	595	600
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Ile Asp Ser Val Cys Ala Ser Tyr Phe		620
625	630	

<210> 10

<211> 1905

<212> DNA

<213> Artificial sequence

<220>

<223> Colicin Ia attached to Pheromone peptide from
Staphylococcus epidermidis

<400> 10

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aataagttct ggggtattga ttccgtttgt gcatactatt tttaa 1905

<210> 11

<211> 633

<212> PRT

<213> Artificial sequence

<220>

<223> Pheromone peptide from *Staphylococcus aureus* AgrDI
attached to Colicin Ia

<400> 11

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			20					25					30		
Ala	Val	Asp	Ile	Tyr	Val	Asn	Pro	Pro	Arg	Val	Asp	Val	Phe	His	Gly
		35				40					45				
Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	Gly
	50				55						60				
Asn	Glu	Trp	Val	Asp	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	Glu	Lys	Arg
65					70				75					80	
Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	Gln	Lys
			85					90					95		
Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	Ala	Ala
			100				105					110			
Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	Arg	Ala
	115					120						125			
Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	Leu	Leu
	130					135					140				
Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	Gly	Tyr
145					150				155					160	
Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	Asp	Ala
			165					170					175		
Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	Glu	Gln
		180					185					190			
Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	Ala	Ala
	195					200					205				
Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	Thr	Arg
	210					215				220					
Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	Leu	Asp
225					230				235					240	
Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	Arg	Ala

				245					250					255			
Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	Leu	Asn		
			260					265					270				
Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	Gln	Gln		
			275				280						285				
Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	Phe	Pro		
			290				295				300						
Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	Pro	Arg		
305					310					315					320		
Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	Asn	Arg		
				325					330					335			
Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	Lys	Arg		
			340					345					350				
Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	Glu	Gly		
			355				360					365					
Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Glu	Trp	Asp	Lys	Leu	Arg		
			370			375					380						
Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	Ala	Glu	Ser	Ala		
385					390					395					400		
Val	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	Arg	Thr	Asn	Glu	Gln	Lys		
				405					410					415			
His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	Lys	Glu	Lys	Glu	Asn	Ile		
			420				425						430				
Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	Ile	Ala	Glu	Glu	Lys	Arg		
			435				440					445					
Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	Ala	Ile	Asn	Phe	Thr	Thr		
			450			455					460						
Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	Gly	Ala	Lys	Ala	Glu	Gln		
465					470					475					480		
Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	Gly	Lys	Lys	Ile	Arg	Asn		
				485				490						495			
Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	Tyr	Arg	Ala	Asp	Ile	Asn		
			500					505					510				
Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala	Ile	Ala	Ala	Ala	Leu	Glu		
			515				520					525					
Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn	Leu	Asn	Arg	Phe	Ser	Arg		
			530			535					540						
Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser	Leu	Ala	Asp	Trp	Ile	Thr		
545					550					555					560		
Glu	Phe	Gly	Lys	Ala	Val	Arg	Thr	Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val		
				565				570						575			
Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly	Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala		
				580				585					590				
Leu	Val	Phe	Ser	Ile	Leu	Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr		
			595			600					605						
Gly	Leu	Leu	Met	Ala	Val	Thr	Gly	Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val		
			610			615					620						
Glu	Lys	Ala	Asn	Lys	Phe	Trp	Gly	Ile									
625					630												

<210> 12

<211> 1905

<212> DNA

<213> Artificial sequence

<220>

<223> Pheromone peptide from *Staphylococcus aureus* AgrDI
attached to Colicin Ia

<400> 12

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cctccacgtg tcgatgtctt tcatgggtacc ccgcctgcat ggagttcctt cgggaacaaa 180
accatctggg gcggaacga gtgggttgat gattcccca cccgaagtga tatcgaaaaa 240
agggacaagg aaatcacagc gtacaaaaaac acgctcagcg cgcagcagaa agagaatgag 300
aataagcgta ctgaagccgg aaaacgcctc tctgcggcga ttgctgcaag ggaaaaagat 360
gaaaacacac tgaaaacact ccgtgccgga aacgcagatg ccgctgatat tacacgacag 420
gagttcagac tcctgcaggc agagctgaga gaatacggat tccgtactga aatcgccgga 480
tatgacgccc tccggctgca tacagagagc cggatgctgt ttgctgatgc tgattctctt 540
cgtatatctc cccgggaggc caggtcgtta atcgaacagg ctgaaaaacg gcagaaggat 600
gcgcagaacg cagacaagaa ggccgctgat atgcttgctg aatacgagcg cagaaaaggt 660
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gatgcacaac agggccgtct gctcgggcag cagacacgga atgacagggc catttcagag 780
gcccggaata aactcagttc agtgacggaa tcgcttaaca cggcccgtaa tgcattaacc 840
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accatcatag caggcaatgc cgcaacggct cttgtggcac tggcttcag tattcttacc 1800
ggaagcgctt taggcattat cgggtatggt ttactgatgg ctgtcaccgg tgcgctgatt 1860
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<210> 13

<211> 651

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin Ia attached to Pheromone peptide from
Staphylococcus epidermidis

<400> 13

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Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
20     25     30
Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His Gly
35     40     45
Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly Gly
50     55     60
Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile Glu
65     70     75     80
Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala Gln
85     90     95
Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu Ser
100    105    110
Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr Leu
115    120    125
Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe Arg
130    135    140

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Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	145	150	155	160
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	165	170	175	
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	180	185	190	
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	195	200	205	
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	210	215	220	
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	225	230	235	240
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	245	250	255	
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	260	265	270	
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	275	280	285	
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	290	295	300	
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	305	310	315	320
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	325	330	335	
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	340	345	350	
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	355	360	365	
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	370	375	380	
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	385	390	395	400
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	405	410	415	
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	420	425	430	
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	435	440	445	
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	450	455	460	
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	465	470	475	480
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	485	490	495	
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	500	505	510	
Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala	515	520	525	
Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn	530	535	540	
Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser	545	550	555	560
Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly	Thr	565	570	575	
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly	580	585	590	
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile	Leu	595	600	605	
Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala	Val	610	615	620	

<220>
<223> Colicin Ia attached to Pheromone peptide from
Staphylococcus epidermidis

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<210> 15
<211> 660
<212> PRT
<213> Artificial sequence
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<400> 15
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1 5 10 15

Gly	Tyr	Asp	Ser	Asp	Gly	His	Glu	Ile	Met	Ala	Val	Ala	Ser	Pro	Ile	
			20					25						30		
Tyr	Val	Ala	Ser	Asn	Pro	Pro	Arg	Val	Ala	Ser	Pro	Val	Phe	His	Gly	
		35					40					45				
Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	Gly	
	50					55					60					
Asn	Glu	Trp	Val	Ala	Ser	Pro	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	Glu	
65					70					75					80	
Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	
				85					90					95		
Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	
			100					105					110			
Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	
		115					120					125				
Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	
	130					135					140					
Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	
145					150					155					160	
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	
				165					170					175		
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	
			180					185					190			
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	
		195					200					205				
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	
	210					215					220					
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	
225					230					235					240	
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	
			245						250					255		
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	
		260					265						270			
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	
	275					280						285				
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	
	290					295					300					
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	
305					310					315					320	
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	
			325						330					335		
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	
		340					345					350				
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	
	355					360						365				
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	
	370					375					380					
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	
385					390					395					400	
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	
			405						410					415		
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	
		420						425					430			
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	
	435						440					445				
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	
	450					455					460					
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	
465					470					475					480	
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	
			485						490					495		
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	

[illegible]

<210> 16

<211> 1929

<212> DNA

<213> Artificial sequence

<220>

<223> colicin Ia attached to streptococcus pneumoniae
polypeptide pheromone

<400> 16

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ggtaccccg	ctgcatggag	ttccttcggg	aacaaaacca	tctggggcgg	aaacgagtg	180
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aaaaacacg	tcagcgcgca	gcagaaagag	aatgagaata	agcgactga	agccggaaaa	300
cgctctctg	cggcgattgc	tgcaagggaa	aaagatgaaa	acacactgaa	aacactccgt	360
gccggaaaac	cagatgccgc	tgatattaca	cgacaggagt	tcagactcct	gcaggcagag	420
ctgagagaat	acggattccg	tactgaaatc	gccggatatg	acgcccctcg	gctgcataca	480
gagagccgga	tgctgtttgc	tgatgtgat	tcctctcgta	tatctccccg	ggaggccagg	540
tcgttaatcg	aacaggctga	aaaacggcag	aaggatg	agaacgcaga	caagaaggcc	600
gctgatatgc	ttgctgaata	cgagcgcaga	aaaggatttc	tggaaccccc	gttgtcagag	660
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ctggactata	aacgcaatat	tctgaattgac	cggaaatccgg	tggtgcagaga	ggatgtggaa	1080
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cttgatgcc	gaaataaaat	cacctctgct	gaatctgcgg	taaattcggc	gagaaataac	1200
ctcagtgcca	gaacaaatga	gcaaaagcat	gcaaatgacg	ctcttaaatgc	cctgttgaag	1260
gaaaaagaga	atatacgtaa	ccagctttcc	ggcatcaatc	agaagatagc	ggaagagaaa	1320
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acggctcttg tggcactggg cttcagattt cttaccggaa gcgcttttagg cattatcggg 1800
tatggtttac tgatggctgt caccgggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattga gatgaggttg tcaaaattct tccgtgattt tattttacaa 1920
agaaaaaag                                     1929

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<210> 17

<211> 650

<212> PRT

<213> Artificial sequence

<220>

<223> Colicin Ia linked to E. facaelis pheromone cCF10

<400> 17

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Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
20     25     30
Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His Gly
35     40     45
Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly Gly
50     55     60
Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile Glu
65     70     75     80
Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala Gln
85     90     95
Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu Ser
100    105    110
Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr Leu
115    120    125
Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe Arg
130    135    140
Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly Phe Arg Thr Glu Ile Ala
145    150    155    160
Gly Tyr Asp Ala Leu Arg Leu His Thr Glu Ser Arg Met Leu Phe Ala
165    170    175
Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg Glu Ala Arg Ser Leu Ile
180    185    190
Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala Gln Asn Ala Asp Lys Lys
195    200    205
Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg Arg Lys Gly Ile Leu Asp
210    215    220
Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly Gly Ala Ala Leu Ala Val
225    230    235    240
Leu Asp Ala Gln Gln Ala Arg Leu Leu Gly Gln Gln Thr Arg Asn Asp
245    250    255
Arg Ala Ile Ser Glu Ala Arg Asn Lys Leu Ser Ser Val Thr Glu Ser
260    265    270
Leu Asn Thr Ala Arg Asn Ala Leu Thr Arg Ala Glu Gln Gln Leu Thr
275    280    285
Gln Gln Lys Asn Thr Pro Asp Gly Lys Thr Ile Val Ser Pro Glu Lys
290    295    300
Phe Pro Gly Arg Ser Ser Thr Asn His Ser Ile Val Val Ser Gly Asp
305    310    315    320
Pro Arg Phe Ala Gly Thr Ile Lys Ile Thr Thr Ser Ala Val Ile Asp
325    330    335
Asn Arg Ala Asn Leu Asn Tyr Leu Leu Ser His Ser Gly Leu Asp Tyr
340    345    350
Lys Arg Asn Ile Leu Asn Asp Arg Asn Pro Val Val Thr Glu Asp Val

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355					360					365					
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp
370					375					380					
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser
385	390					395					400				
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala
405					410					415					
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu
420					425					430					
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys
435					440					445					
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp
450					455					460					
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr
465	470					475					480				
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys
485					490					495					
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys
500					505					510					
Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala
515					520					525					
Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn
530					535					540					
Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser
545	550					555					560				
Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly	Thr
565					570					575					
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly
580					585					590					
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile	Leu
595					600					605					
Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala	Val
610					615					620					
Thr	Gly	Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys	Phe
625	630					635					640				
Trp	Gly	Ile	Leu	Val	Thr	Leu	Val	Phe	Val						
645					650										

<210> 18

<211> 1899

<212> DNA

<213> Artificial sequence

<220>

<223> Colicin Ia linked to E. facaelis pheromone cCF10

<400> 18

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ggtaccccg cctgcatggag ttccttcggg aacaaaacca tctggggcgg aaacgagtgg 180
gttgatgatt cccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtactga agccggaaaa 300
cgcctctctg cggcgattgc tgcaagggaa aaagatgaaa acacactgaa aacactccgt 360
gccggaaacg cagatgccgc tgatattaca cgacaggagt tcagactcct gcaggcagag 420
ctgagagaat acggattccg tactgaaatc gccggatatg acgcctccg gctgcataca 480
gagagccgga tctgttttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540
tcgttaatcg aacaggctga aaaacggcag aaggatgcgc agaacgcaga caagaaggcc 600
gctgatatgc ttgctgaata cgagcgcaga aaaggtattc tggacacccg gttgtcagag 660
ctggaaaaaa atggcggggc agcccttgcc gttcttgatg cacaacaggc ccgtctgctc 720
gggcagcaga cacggaatga cagggccatt tcagaggccc ggaataaact cagttcagtg 780

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acggaatcgc ttaacacggc ccgtaatgca ttaaccagag ctgaacaaca gctgacgcaa 840
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tcaacaaatc attctattgt tgtgagcggg gatccgagat ttgccggtag gataaaaaatc 960
acaaccagcg cagtcacgca taaccgtgca aacctgaatt atcttctgag ccattccggg 1020
ctggactata aacgcaatat tctgaatgac cggaatccgg tggtagacaga ggatgtggaa 1080
ggtgacaaga aaatttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
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ctcagtgccg gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcatacaatc agaagatagc ggaagagaaa 1320
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gagtctgtga agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620
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acggctcttg tggcactggg cttcagtatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattct tgtcacgctt gtcttcgctc 1899

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<210> 19

<211> 678

<212> PRT

<213> Artificial sequence

<220>

<223> colicin Ia attached to G28-V50/E216-S228 from

HBsAg ScFv

<400> 19

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Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu
 1           5           10           15
Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
          20           25           30
Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His Gly
          35           40           45
Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly Gly
          50           55           60
Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile Glu
65           70           75           80
Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala Gln
          85           90           95
Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu Ser
          100          105          110
Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr Leu
          115          120          125
Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe Arg
          130          135          140
Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly Phe Arg Thr Glu Ile Ala
145          150          155          160
Gly Tyr Asp Ala Leu Arg Leu His Thr Glu Ser Arg Met Leu Phe Ala
          165          170          175
Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg Glu Ala Arg Ser Leu Ile
          180          185          190
Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala Gln Asn Ala Asp Lys Lys
          195          200          205
Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg Arg Lys Gly Ile Leu Asp
          210          215          220
Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly Gly Ala Ala Leu Ala Val
225          230          235          240
Leu Asp Ala Gln Gln Ala Arg Leu Leu Gly Gln Gln Thr Arg Asn Asp

```

				245					250					255	
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser
			260					265					270		
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr
			275					280					285		
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys
			290				295				300				
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp
305					310					315					320
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp
				325					330					335	
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr
			340					345					350		
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val
			355				360					365			
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp
			370			375				380					
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser
385					390					395					400
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala
				405					410					415	
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu
			420					425					430		
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys
			435				440					445			
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp
			450			455					460				
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr
465					470					475					480
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys
				485					490					495	
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys
			500					505					510		
Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala
			515				520					525			
Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn
			530			535					540				
Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser
545					550					555					560
Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly	Thr
				565					570					575	
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly
			580					585					590		
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile	

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<210> 20
<211> 2034
<212> DNA
<213> Artificial sequence
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<220>

<223> colicin Ia attached to G28-V50/E216-S228 from
HBsAg ScFv

<400> 20

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ggccatgaaa ttatggccgt tgatatttat gtaaaccctc cacgtgtcga tgtctttcat 120
ggtaccccg cgtcatggag ttccttcggg aacaaaacca tctggggcgg aaacgagtg 180
gttgatgatt cccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtactga agccggaaaa 300
cgctctctcg cggcgattgc tgcaaggga aaagatgaaa acacactgaa aacactccgt 360
gccggaaacg cagatgccgc tgatattaca cgacaggagt tcagactcct gcaggcagag 420
ctgagagaat acggattccg tactgaaatc gccggatatg acgccctccg gctgcataca 480
gagagccgga tgctgtttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540

tcgttaatcg aacaggctga aaaacggcag aaggatgcgc agaacgcaga caagaaggcc 600
gctgatatgc ttgctgaata cgagcgcaga aaaggatttc tggacacccg gttgtcagag 660
ctggaaaaaa atggcggggc agcccttgcc gttcttgatg cacaacaggc ccgtctgctc 720
gggcagcaga caggaatga cagggccatt tcagaggccc ggaataaact cagttcagtg 780
acggaatcgc ttaacacggc ccgtaatgca ttaaccagag ctgaacaaca gctgacgcaa 840
cagaaaaaca cgctgcacgg caaaacgata gtttccccctg aaaaattccc gggcgcttca 900
tcaacaaatc attctattgt tgtgagcggg gatccgagat ttgccggtac gataaaaaatc 960
acaaccagcg cagtcacgca taaccgtgca aacctgaatt atcttctgag ccattccggg 1020
ctggactata aacgcaatat tctgaatgac cggaatccgg tggtgacaga ggatgtggaa 1080
ggtgacaaga aaatttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
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ctcagtgcca gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcacatc atcagaatagc ggaagagaaa 1320
agaaaacagg atgaactgaa ggcaacgaaa gacgcaatta atttcacaac agagttcctg 1380
aaatcagttt cagaaaaata tgggtgcaaaa gctgagcagt tagccagaga gatggccggg 1440
caggctaaag ggaagaaaat acgtaatgtt gaagaggcat taaaaacgta tgaaaagtac 1500
cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgcagccctt 1560
gagtctgtga agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620
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acagagaact ggcgtcctct ttttggttaa acagaaacca tcatagcagg caatgccgca 1740
acggctcttg tggcactggt cttcagatatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattgg attcaccttc agtgactact acatgagctg gatccgccag 1920
gctccaggga aggggctgga gtgggttgaa gatgaggctg actattactg taactcccgg 1980
gacagcagtg gtgaagatga ggctgactat tactgtaact cccgggacag cagt 2034

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<210> 21

<211> 656

<212> PRT

<213> Artificial sequence

<220>

<223> colicin Ia and the C. albicans mating pheromone

<400> 21

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Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu
 1           5           10           15
Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
          20           25           30
Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His Gly
          35           40           45
Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly Gly
          50           55           60
Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile Glu
65           70           75           80

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Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	
				85					90					95		
Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	
			100					105					110			
Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	
		115				120						125				
Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	
	130					135					140					
Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	
145					150					155					160	
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	
			165						170					175		
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	
			180					185					190			
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	
		195					200					205				
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	
	210					215					220					
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	
225					230					235					240	
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	
			245						250					255		
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	
		260						265					270			
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	
	275						280					285				
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	
	290					295					300					
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	
305					310					315					320	
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	
			325						330					335		
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	
		340					345						350			
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	
		355				360						365				
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	
	370					375					380					
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	
385					390					395					400	
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	
			405						410					415		
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	
		420						425					430			
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	
	435						440					445				
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	
	450					455					460					
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	
465					470					475					480	
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	
			485						490					495		
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	
		500					505						510			
Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala	
	515						520					525				
Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn	
	530					535					540					
Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser	
545					550					555					560	
Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly	Thr	

<220>
<223> colicin Ia and the *C. albicans* mating pheromone

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<210> 23
<211> 8
<212> PRT
<213> S. Aurues
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-25-

Tyr Ser Thr Cys Asp Phe Ile Met
 1 5

<210> 24
 <211> 11
 <212> PRT
 <213> S. Aurues

<400> 24
 Gly Val Ala Ser Asn Ala Cys Ser Ser Leu Phe
 1 5 10

<210> 25
 <211> 8
 <212> PRT
 <213> S. Aurues

<400> 25
 Tyr Ile Asn Cys Asp Phe Leu Leu
 1 5

<210> 26
 <211> 8
 <212> PRT
 <213> S. Aurues

<400> 26
 Tyr Ser Thr Cys Phe Phe Ile Met
 1 5

<210> 27
 <211> 8
 <212> PRT
 <213> S. epidermis

<400> 27
 Asp Ser Val Cys Ala Ser Tyr Phe
 1 5

<210> 28
 <211> 43
 <212> PRT
 <213> S. Pneumoniae

<400> 28
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 1 5 10 15
 Glu Lys Asp Leu Gln Lys Ile Lys Gly Gly Glu Met Arg Leu Ser Lys
 20 25 30
 Phe Phe Arg Asp Phe Ile Leu Gln Arg Lys Lys
 35 40

<210> 29
 <211> 7
 <212> PRT

<213> E. Facaelis

<400> 29

Leu Val Thr Leu Val Phe Val

1

5

<210> 30

<211> 644

<212> PRT

<213> E. coli

<400> 30

Met	Ser	Asp	Pro	Val	Ala	Arg	Gly	Ile	Thr	Asn	Pro	Gly	Ala	Glu	Ser	1	5	10	15
Leu	Gly	Tyr	Asp	Ser	Asp	Gly	His	Glu	Ile	Met	Ala	Val	Ala	Ser	Pro	20	25	30	
Ile	Tyr	Val	Ala	Ser	Asn	Pro	Pro	Arg	Val	Ala	Ser	Pro	Val	Phe	His	35	40	45	
Gly	Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	50	55	60	
Gly	Asn	Glu	Trp	Val	Ala	Ser	Pro	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	65	70	75	80
Glu	Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	85	90	95	
Gln	Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	100	105	110	
Ser	Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	115	120	125	
Leu	Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	130	135	140	
Arg	Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	145	150	155	160
Ala	Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	165	170	175	
Ala	Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	180	185	190	
Ile	Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	195	200	205	
Lys	Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	210	215	220	
Asp	Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	225	230	235	240
Val	Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	245	250	255	
Asp	Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	260	265	270	
Ser	Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	275	280	285	
Thr	Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	290	295	300	
Lys	Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	305	310	315	320
Asp	Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	325	330	335	
Asp	Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	340	345	350	
Tyr	Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	355	360	365	
Val	Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu				

370	375	380
Trp Asp Lys Leu Arg Gln Arg Leu Leu Asp Ala Arg Asn Lys Ile Thr		
385	390	395
Ser Ala Glu Ser Ala Val Ala Ser Asn Ser Ala Arg Asn Asn Leu Ser		400
	405	410
Ala Arg Thr Asn Glu Gln Lys His Ala Asn Asp Ala Leu Asn Ala Leu		415
	420	425
Leu Lys Glu Lys Glu Asn Ile Arg Asn Gln Leu Ser Gly Ile Asn Gln		430
	435	440
Lys Ile Ala Glu Glu Lys Arg Lys Gln Asp Glu Leu Lys Ala Thr Lys		445
	450	455
Asp Ala Ile Asn Phe Thr Thr Glu Phe Leu Lys Ser Val Ser Glu Lys		460
465	470	475
Tyr Gly Ala Lys Ala Glu Gln Leu Ala Arg Glu Met Ala Gly Gln Ala		480
	485	490
Lys Gly Lys Lys Ile Arg Asn Val Glu Glu Ala Leu Lys Thr Tyr Glu		495
	500	505
Lys Tyr Arg Ala Asp Ile Asn Lys Lys Ile Asn Ala Lys Asp Arg Ala		510
	515	520
Ala Ile Ala Ala Ala Leu Glu Ser Val Lys Leu Ser Asp Ile Ser Ser		525
	530	535
Asn Leu Asn Arg Phe Ser Arg Gly Leu Gly Tyr Ala Gly Lys Phe Thr		540
545	550	555
Ser Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Ala Arg Gly		560
	565	570
Thr Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala		575
	580	585
Gly Asn Ala Ala Thr Ala Leu Val Ala Leu Ala Leu Val Phe Ser Ile		590
	595	600
Leu Thr Gly Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala		605
	610	615
Val Thr Gly Ala Leu Ile Asp Glu Ser Leu Val Glu Lys Ala Asn Lys		620
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Phe Trp Gly Ile		640

<210> 31

<211> 1878

<212> DNA

<213> E. coli

<400> 31

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gttgatgatt	ccccaacccg	aagtgatatc	gaaaaaagg	acaaggaaat	cacagcgta	240
aaaaacacgc	tcagcgcgca	gcagaaagag	aatgagaata	agcgactga	agccggaaaa	300
cgcctctctg	cggcgattgc	tgcaagggaa	aaagatgaaa	acacactgaa	aacactccgt	360
gccggaaacg	cagatgccgc	tgatattaca	cgacaggagt	tcagactcct	gcaggcagag	420
ctgagagaat	acggattccg	tactgaaatc	gccggatatg	acgccctccg	gctgcataca	480
gagagccgga	tgctgtttgc	tgatgctgat	tctcttcgta	tatctccccg	ggaggccagg	540
tcgttaatcg	aacaggctga	aaaacggcag	aaggatgcgc	agaacgcaga	caagaaggcc	600
gctgatatgc	ttgctgaata	cgagcgcgca	aaaggatttc	tggaaccccc	gttgtcagag	660
ctggaaaaaa	atggcggggc	agcccttgcc	gttcttgatg	cacaacaggc	ccgtctgctc	720
gggcagcaga	caggaatgca	cagggccatt	tcagaggccc	ggaataaact	cagttcagt	780
acggaatcgc	ttaacacggc	ccgtaatgca	ttaaccagag	ctgaacaaca	gctgacgcaa	840
cagaaaaaca	cgccctgacg	caaaacgata	gtttccctcg	aaaaattccc	ggggcgttca	900
tcaacaaatc	attctattgt	tgtgagcgg	gatccgagat	ttgccggtac	gataaaaaatc	960
acaaccagcg	cagtcacgca	taaccgtgca	aacctgaatt	atcttctgag	ccattccggt	1020
ctggactata	aacgcaatat	tctgaatgac	cggaatccgg	tggtgacaga	ggatgtggaa	1080

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ggtgacaaga aaatttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
cttgatgcc aaaaataaaat cacctctgct gaactctgcg taaattcggc gagaaataac 1200
ctcagtgcc gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcatacatc agaagatagc ggaagagaaa 1320

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agaaaacagg atgaactgaa ggcaacgaaa gacgcaatta atttcacaac agagttcctg 1380
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caggctaaag ggaagaaaaat acgtaatgtt gaagaggcat taaaaacgta tgaaaagtac 1500
cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgcagccctt 1560
gagtctgtga agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620
tatgcaggaa aatttacaag tcttgctgac tggatcactg agtttggtta ggctgtccgg 1680
acagagaact ggcgtcctct ttttgttaaa acagaaacca tcatagcagg caatgccgca 1740
acggctcttg tggcactggg cttcagtatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccgggtgc ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtatt 1878

```

<210> 32

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> HBV PreS1 scFV linked to a pore-forming region of Colicin Ia

<400> 32

```

Lys Phe Thr Ser Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val
 1      5      10      15
Ala Arg Gly Thr Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr
      20      25      30
Ile Ile Ala Gly Asn Ala Ala Thr Ala Leu Val Ala Leu Ala Leu Val
      35      40      45
Phe Ser Ile Leu Thr Gly Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu
      50      55      60
Leu Met Ala Val Thr Gly Ala Leu Ile Asp Glu Ser Leu Val Glu Lys
      65      70      75      80
Ala Asn Lys Phe Trp Gly Ile Gln Met Gln Leu Val Gln Ser Gly Ala
      85      90      95
Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
      100     105     110
Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Ala Arg Gly Gln
      115     120     125
Ala Ala Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Lys Phe
      130     135     140
Gly Thr Pro Asn Tyr Ile Gln Lys Phe Gln Gly Arg Val Thr Ile Thr
      145     150     155     160
Ala Asp Lys Ser Thr Thr Ala Tyr Met Glu Leu Lys Asn Leu Arg
      165     170     175
Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Ser Gly Gly
      180     185     190
Ala Glu Tyr Tyr Asn Gly Leu Asp Val Ser Gly Gly Gly Gly Ser Gly
      195     200     205
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro
      210     215     220
Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser
      225     230     235     240
Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln
      245     250     255
Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg
      260     265     270
Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser

```

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      275              280              285
Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr
      290              295              300
Tyr Cys Ala Ala Trp Asp Asp Ser Leu His Ala Arg Val Phe Gly Gly
      305              310              315              320
Gly Thr

```

<210> 33

<211> 976

<212> DNA

<213> Artificial sequence

<220>

<223> HBV PreS1 scFV linked to a pore-forming region of Colicin Ia

<400> 33

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tggcgctctc tttttgttaa aacagaaacc atcatagcag gcaatgccgc aacggctctt 120
gtggcactgg tcttcagtat tcttaccgga agcgcttttag gcattatcgg gtatggttta 180
ctgatggctg tcaccggtgc gctgattgat gaatcgcttg tggaaaaagc gaataagttc 240
tggggatttg attccgtttg tgcctcctat ttttaacaga tgcagctggt gcagtctggg 300
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 360
ttcagcagct atgctatcag ctgggtgcga caggccgctg gacaagggct tgagtggatg 420
ggagggatca tacctaaatt tggtagacca aactacatac agaagttcca gggcagagtc 480
acgattaccg cggacaagtc cacgaccaca gcctacatgg agctgaagaa cctgagatct 540
gaggacacgg ccgtatatta ctgtgcgaga aacgggtcag ggggagccga atactacaac 600
ggtttggacg tctccggtgg aggcgggttc ggcggaggtg gctctggtgg aggcggtagt 660
cagtcctgtg tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 720
tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc 780
ccaggaacgg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 840
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg 900
tccgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgca tgctcgtgta 960
ttcggcggag ggacca 976

```

<210> 34

<211> 879

<212> PRT

<213> Artificial sequence

<220>

<223> HBV PreS1 scFV linked to Colicin Ia

<400> 34

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Met Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser
 1              5              10              15
Leu Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro
      20              25              30
Ile Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His
      35              40              45
Gly Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly
      50              55              60
Gly Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile
      65              70              75              80
Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala
      85              90              95
Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu
      100              105              110
Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr

```

		115					120					125				
Leu	Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	
	130					135					140					
Arg	Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	
145					150					155					160	
Ala	Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	
				165					170					175		
Ala	Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	
			180					185					190			
Ile	Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	
		195					200					205				
Lys	Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	
	210					215					220					
Asp	Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	
225					230					235					240	
Val	Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	
				245					250					255		
Asp	Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	
			260					265					270			
Ser	Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	
		275					280					285				
Thr	Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	
	290					295					300					
Lys	Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	
305					310					315					320	
Asp	Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	
				325					330					335		
Asp	Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	
			340					345					350			
Tyr	Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	
		355					360					365				
Val	Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	
	370					375					380					
Trp	Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	
385					390					395					400	
Ser	Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	
				405					410					415		
Ala	Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	
			420					425					430			
Leu	Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	
		435					440					445				
Lys	Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	
	450					455					460					
Asp	Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	
465																

Leu	Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala
610						615					620				
Val	Thr	Gly	Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys
625					630					635					640
Phe	Trp	Gly	Ile	Gln	Met	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys
				645					650						655
Lys	Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr
			660					665					670		
Phe	Ser	Ser	Tyr	Ala	Ile	Ser	Trp	Val	Ala	Arg	Gly	Gln	Ala	Ala	Gly
		675					680					685			
Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Ile	Ile	Pro	Lys	Phe	Gly	Thr	Pro
	690					695					700				
Asn	Tyr	Ile	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys
705					710					715					720
Ser	Thr	Thr	Thr	Ala	Tyr	Met	Glu	Leu	Lys	Asn	Leu	Arg	Ser	Glu	Asp
				725					730					735	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Gly	Ser	Gly	Gly	Ala	Glu	Tyr
			740					745					750		
Tyr	Asn	Gly	Leu	Asp	Val	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly
		755					760					765			
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala
	770					775					780				
Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser
785					790					795					800
Ser	Asn	Ile	Gly	Ser	Asn	Tyr	Val	Tyr	Trp	Tyr	Gln	Gln	Leu	Pro	Gly
				805					810					815	
Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Arg	Asn	Asn	Gln	Arg	Pro	Ser	Gly
			820					825					830		
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu
		835					840					845			
Ala	Ile	Ser	Gly	Leu	Arg	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala
	850					855					860				
Ala	Trp	Asp	Asp	Ser	Leu	His	Ala	Arg	Val	Phe	Gly	Gly	Gly	Thr	
865					870					875					

<210> 35

<211> 2578

<212> DNA

<213> Artificial sequence

<220>

<223> HBV PreS1 scFV linked to Colicin Ia

<400> 35

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ggccatgaaa	ttatggccgt	tgatatttat	gtaaaccctc	cacgtgtcga	tgtctttcat	120
ggtaccccg	ctgcatggag	ttccttcggg	aacaaaacca	tctggggcgg	aaacgagtgg	180
ggtgatgatt	ccccaacccg	aagtgatatc	gaaaaaagg	acaaggaaat	cacagcgtac	240
aaaaacacgc	tcagcgcgca	gcagaaagag	aatgagaata	agcgtactga	agccggaaaa	300
cgcctctctg	cggcgattgc	tgcaagggaa	aaagatgaaa	acacactgaa	aacactccgt	360
gccggaaacg	cagatgccgc	tgatattaca	cgacaggagt	tcagactcct	gcaggcagag	420
ctgagagaat	acggattccg	tactgaaatc	gccggatatg	acgccctccg	gctgcataca	480
gagagccgga	tgtctgtttg	tgatgctgat	tctcttcgta	tatctccccg	ggaggccagg	540
tcgttaatcg	aacaggctga	aaaacggcag	aaggatgcgc	agaacgcaga	caagaaggcc	600
gctgatatgc	ttgctgaata	cgagcgcaga	aaaggtattc	tggacaccgg	ggtgtcagag	660
ctggaaaaaa	atggcggggc	agcccttgcc	gttcttgatg	cacaacaggc	ccgtctgctc	720
gggcagcaga	cacggaatga	cagggccatt	tcagaggccc	ggaataaaact	cagttcagtg	780
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cagaaaaaca	cgcttgacgg	caaaacgata	gtttcccctg	aaaaattccc	ggggcgttca	900
tcaacaaatc	attctattgt	tgtgagcggg	gatccgagat	ttgccgggtac	gataaaaaatc	960


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acaaccagcg cagtcacgca taaccgtgca aacctgaatt atcttctgag ccattccggt 1020
ctggactata aacgcaatat tctgaatgac cggaatccgg tggtagacaga ggatgtggaa 1080
ggtgacaaga aaatttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
cttgatgcca gaaataaaat cacctctgct gaatctgagg taaattcggc gagaaataac 1200
ctcagtacca gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcatacaatc agaagatagc ggaagagaaa 1320
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cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgcagccctt 1560
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aataagttct ggggtattca gatgcagctg gtgcagtcgt gggctgagggt gaagaagcct 1920
gggtcctcgg tgaaggctct ctgcaaggct tctggaggca ccttcagcag ctatgctatc 1980
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tactgtcgga gaaacgggtc agggggagcc gaatactaca acggtttgga cgtctccggg 2220
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ctcctcatct ataggaataa tcagcggccc tcaggggtcc ctgaccgatt ctctggctcc 2460
aagtctggca cctcagcctc cctggccatc agtgggctcc ggtccgagga tgaggctgat 2520
tattactgtg cagcatggga tgacagcctg catgctcgtg tattcggcgg agggacca 2578

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<210> 36

<211> 679

<212> PRT

<213> Artificial sequence

<220>

<223> G28 - V50/E217 - S228 of HBsAg ScFV linked to
colicin Ia

<400> 36

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Met Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser
 1               5               10               15
Leu Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro
 20               25               30
Ile Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His
 35               40               45
Gly Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly
 50               55               60
Gly Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile
 65               70               75               80
Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala
 85               90               95
Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu
 100              105              110
Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr
 115              120              125
Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe
 130              135              140
Arg Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly Phe Arg Thr Glu Ile
 145              150              155              160
Ala Gly Tyr Asp Ala Leu Arg Leu His Thr Glu Ser Arg Met Leu Phe
 165              170              175
Ala Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg Glu Ala Arg Ser Leu

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			180					185					190				
Ile	Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys		
		195					200					205					
Lys	Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu		
	210					215					220						
Asp	Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala		
225					230					235					240		
Val	Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn		
			245						250					255			
Asp	Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu		
		260						265					270				
Ser	Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu		
	275						280					285					
Thr	Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu		
	290					295					300						
Lys	Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly		
305					310					315					320		
Asp	Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile		
			325						330					335			
Asp	Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp		
		340						345					350				
Tyr	Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp		
	355						360					365					
Val	Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu		
	370					375					380						
Trp	Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr		
385					390					395					400		
Ser	Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser		
			405					410						415			
Ala	Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu		
		420						425					430				
Leu	Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln		
	435					440						445					
Lys	Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys		
	450					455					460						
Asp	Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys		
465					470					475					480		
Tyr	Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala		
			485					490						495			
Lys	Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu		
		500						505					510				
Lys	Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala		
	515						520					525					
Ala	Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser		
	530					535					540						
Asn	Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr		
545					550					555					560		
Ser	Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly		
			565					570						575			
Thr	Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala		
		580						585					590				
Gly	Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile		
		595						600					605				
Leu	Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala		
	610					615					620						
Val	Thr	Gly	Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys		
625					630					635					640		
Phe	Trp	Gly	Ile	Gly	Phe	Thr	Phe	Ser	Asp	Tyr	Tyr	Met	Ser	Trp	Ile		
			645						650					655			

<220>
<223> G28 - V50/E217 - S228 of HBsAg ScFv linked to colicin Ia

```
<210> 38
<211> 673
<212> PRT
<213> Artificial sequence
```

```
<400> 38
Met Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser
 1             5             10            15
```

```

Leu Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro
      20      25      30
Ile Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His
      35      40      45
Gly Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly
      50      55      60
Gly Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile
      65      70      75      80
Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala
      85      90      95
Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu
      100      105      110
Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr
      115      120      125
Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe
      130      135      140
Arg Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly Phe Arg Thr Glu Ile
      145      150      155      160
Ala Gly Tyr Asp Ala Leu Arg Leu His Thr Glu Ser Arg Met Leu Phe
      165      170      175
Ala Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg Glu Ala Arg Ser Leu
      180      185      190
Ile Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala Gln Asn Ala Asp Lys
      195      200      205
Lys Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg Arg Lys Gly Ile Leu
      210      215      220
Asp Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly Gly Ala Ala Leu Ala
      225      230      235      240
Val Leu Asp Ala Gln Ala Arg Leu Leu Gly Gln Gln Thr Arg Asn
      245      250      255
Asp Arg Ala Ile Ser Glu Ala Arg Asn Lys Leu Ser Ser Val Thr Glu
      260      265      270
Ser Leu Asn Thr Ala Arg Asn Ala Leu Thr Arg Ala Glu Gln Gln Leu
      275      280      285
Thr Gln Gln Lys Asn Thr Pro Asp Gly Lys Thr Ile Val Ser Pro Glu
      290      295      300
Lys Phe Pro Gly Arg Ser Ser Thr Asn His Ser Ile Val Val Ser Gly
      305      310      315      320
Asp Pro Arg Phe Ala Gly Thr Ile Lys Ile Thr Thr Ser Ala Val Ile
      325      330      335
Asp Asn Arg Ala Asn Leu Asn Tyr Leu Leu Ser His Ser Gly Leu Asp
      340      345      350
Tyr Lys Arg Asn Ile Leu Asn Asp Arg Asn Pro Val Val Thr Glu Asp
      355      360      365
Val Glu Gly Asp Lys Lys Ile Tyr Asn Ala Glu Val Ala Leu Ala Glu
      370      375      380
Trp Asp Lys Leu Arg Gln Arg Leu Leu Asp Ala Arg Asn Lys Ile Thr
      385      390      395      400
Ser Ala Glu Ser Ala Val Ala Ser Asn Ser Ala Arg Asn Asn Leu Ser
      405      410      415
Ala Arg Thr Asn Glu Gln Lys His Ala Asn Asp Ala Leu Asn Ala Leu
      420      425      430
Leu Lys Glu Lys Glu Asn Ile Arg Asn Gln Leu Ser Gly Ile Asn Gln
      435      440      445
Lys Ile Ala Glu Glu Lys Arg Lys Gln Asp Glu Leu Lys Ala Thr Lys
      450      455      460
Asp Ala Ile Asn Phe Thr Thr Glu Phe Leu Lys Ser Val Ser Glu Lys
      465      470      475      480
Tyr Gly Ala Lys Ala Glu Gln Leu Ala Arg Glu Met Ala Gly Gln Ala
      485      490      495
Lys Gly Lys Lys Ile Arg Asn Val Glu Glu Ala Leu Lys Thr Tyr Glu

```

	500		505		510
Lys Tyr Arg	Ala Asp Ile Asn Lys	Lys Ile Asn Ala Lys	Asp Arg Ala		
	515	520	525		
Ala Ile Ala	Ala Ala Leu Glu Ser Val	Lys Leu Ser Asp	Ile Ser Ser		
	530	535	540		
Asn Leu Asn	Arg Phe Ser Arg Gly Leu	Gly Tyr Ala Gly	Lys Phe Thr		
545	550	555	560		
Ser Leu Ala	Asp Trp Ile Thr Glu Phe	Gly Lys Ala Val	Ala Arg Gly		
	565	570	575		
Thr Glu Asn	Trp Arg Pro Leu Phe Val	Lys Thr Glu Thr	Ile Ile Ala		
	580	585	590		
Gly Asn Ala	Ala Thr Ala Leu Val Ala	Leu Ala Leu Val	Phe Ser Ile		
	595	600	605		
Leu Thr Gly	Ser Ala Leu Gly Ile Ile	Gly Tyr Gly Leu	Leu Met Ala		
	610	615	620		
Val Thr Gly	Ala Leu Ile Asp Glu Ser	Leu Val Glu Lys	Ala Asn Lys		
625	630	635	640		
Phe Trp Gly	Ile Ser Tyr Ala Ile Ser	Trp Val Ala Arg	Gly Gln Ala		
	645	650	655		
Ala Gly Gln	Gly Leu Glu Trp Met Gly	Ala Ala Trp Asp	Asp Ser Leu		
	660	665	670		

His

<210> 39

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> CDRs from HBV PreS-1 ScFv linked to colicin Ia

<400> 39

atgtctgacc	ctgtacgtat	tacaaatccc	ggtgcagaat	cgctggggta	tgattcagat	60
ggccatgaaa	ttatggccgt	tgatatttat	gtaaaccctc	cacgtgtcga	tgtctttcat	120
ggtacccgcg	ctgcatggag	ttccttcggg	aacaaaacca	tctggggcgg	aaacgagtgg	180
gttgatgatt	ccccaacccg	aagtgatatc	gaaaaaagg	acaaggaaat	cacagcgta	240
aaaaaacacg	tcagcgcgca	gcagaaagag	aatgagaata	agcgtactga	agccggaaaa	300
cgcctctctg	cggcgattgc	tgcaagggaa	aaagatgaaa	acacactgaa	aacactccgt	360
gccggaaacg	cagatgccgc	tgatattaca	cgacaggagt	tcagactcct	gcaggcagag	420
ctgagagaat	acggattccg	tactgaaatc	gccggatatg	acgccctccg	gctgcataca	480
gagagccgga	tgctgtttgc	tgatgctgat	tctcttcgta	tatctccccg	ggaggccagg	540
tcgttaatcg	aacaggctga	aaaacggcag	aaggatgcgc	agaacgcaga	caagaaggcc	600
gctgatatgc	ttgctgaata	cgagcgcaga	aaaggtattc	tggaaccccc	gttgtcagag	660
ctggaaaaaa	atggcggggc	agcccttgcc	gttcttgatg	cacaacaggc	ccgtctgctc	720
gggcagcaga	cacggaatga	cagggccatt	tcagaggccc	ggaataaaact	cagttcagtg	780
acggaatcgc	ttaacacggc	ccgtaatgca	ttaaccagag	ctgaacaaca	gctgacgcaa	840
cagaaaaaca	cgcctgacgg	caaaacgata	gtttcccctg	aaaaattccc	ggggcggttc	900
tcaacaaatc	attctattgt	tgtgagcgg	gatccgagat	ttgccgggtac	gataaaaaat	960
acaaccagcg	cagtcacgca	taaccgtgca	aacctgaatt	atcttctgag	ccattccgg	1020
ctggactata	aacgcaatat	tctgaatgac	cggaatccgg	tggtgacaga	ggatgtggaa	1080
ggtgacaaga	aaattttata	tgctgaagtt	gctgaatggg	ataagttacg	gcaaagattg	1140
cttgatgcc	gaaataaaat	cacctctgct	gaatctgcgg	taaattcggc	gagaaataac	1200
ctcagtgcc	gaacaaatga	gcaaaagcat	gcaaatgacg	ctcttaatgc	cctgttgaa	1260
gaaaaagaga	atatacgtaa	ccagctttcc	ggcatcaatc	agaagatagc	ggaagagaaa	1320
agaaaacagg	atgaactgaa	ggcaacgaaa	gacgcaatta	atttcacaac	agagttcctg	1380
aatcagttt	cagaaaaata	tggtgcaaaa	gctgagcagt	tagccagaga	gatggccggg	1440
caggctaaag	ggaagaaaat	acgtaatgtt	gaagaggcat	taaaaacgta	tgaaaagtac	1500
cgggctgaca	ttaacaaaaa	aattaatgca	aaagatcgtg	cagcgattgc	cgcagccctt	1560
gagtctgtga	agctgtctga	tatatcgtct	aatctgaaca	gattcagtcg	gggactggga	1620

```
tatgcaggaa aatttacaag tcttgctgac tggatcactg agtttggttaa ggctgtccgg 1680
acagagaact ggcgtcctct ttttgtaaaa acagaaacca tcatagcagg caatgccgca 1740
acggctcttg tggcactggg cttcagtatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccgggtgc ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattag ctatgctatc agctgggtgc gacaggccgc tggacaaggg 1920
cttgagtgga tgggagcagc atgggatgac agcctgcat 1959
```

```
<210> 40
<211> 18
<212> PRT
<213> Artificial sequence
```

```
<220>
<223> HBV PreS-1 ScFv CDR2 from the heavy chain
```

```
<400> 40
Gly Ile Ile Pro Lys Phe Gly Thr Pro Asn Tyr Ile Gln Lys Phe Gln
 1             5             10             15
Gly Arg
```

```
<210> 41
<211> 8
<212> PRT
<213> Artificial sequence
```

```
<220>
<223> HBV PreS-1 ScFv CDR2 from the light chain
```

```
<400> 41
Tyr Arg Asn Asn Gln Arg Pro Ser
 1             5
```

```
<210> 42
<211> 14
<212> PRT
<213> Artificial sequence
```

```
<220>
<223> HBV PreS-1 ScFv CDR1-CDR2 light chain linker
```

```
<400> 42
Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile
 1             5             10
```

```
<210> 43
<211> 683
<212> PRT
<213> Artificial sequence
```

```
<220>
<223> CDRs from HBV PreS-1 ScFv attached to colicin Ia
```

```
<400> 43
Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu
 1             5             10             15
Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
 20             25             30
```

Tyr	Val	Ala	Ser	Asn	Pro	Pro	Arg	Val	Ala	Ser	Pro	Val	Phe	His	Gly	
		35					40					45				
Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	Gly	
	50					55					60					
Asn	Glu	Trp	Val	Ala	Ser	Pro	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	Glu	
65					70				75						80	
Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	
			85						90					95		
Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	
			100					105					110			
Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	
		115					120					125				
Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	
	130					135					140					
Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	
145					150					155					160	
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	
				165					170					175		
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	
			180					185					190			
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	
		195					200					205				
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	
	210					215					220					
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	
225					230					235					240	
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	
				245					250					255		
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	
			260					265					270			
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	
		275				280						285				
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	
	290					295					300					
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	
305					310					315					320	
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	
				325					330					335		
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	
			340					345					350			
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	
		355					360					365				
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	
	370					375					380					
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	
385					390					395					400	
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	
				405					410					415		
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	
			420					425					430			
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	
		435					440					445				
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	
	450					455					460					
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	
465					470					475					480	
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	
				485					490					495		
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	
			500					505					510			
Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala	

	515						520						525					
Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn			
	530					535					540							
Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser			
545					550					555					560			
Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly	Thr			
				565					570						575			
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly			
			580					585					590					
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile	Leu			
	595					600					605							
Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala	Val			
	610					615					620							
Thr	Gly	Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys	Phe			
625					630					635					640			
Trp	Gly	Ile	Gly	Ile	Ile	Pro	Lys	Phe	Gly	Thr	Pro	Asn	Tyr	Ile	Gln			
				645					650					655				
Lys	Phe	Gln	Gly	Arg	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys			
			660					665					670					
Leu	Leu	Ile	Tyr	Arg	Asn	Asn	Gln	Arg	Pro	Ser								
	675					680												

```
<210> 44
<211> 1998
<212> DNA
<213> Artificial sequence
```

<220>
<223> CDRs from HBV PreS-1 ScFv attached to colicin Ia

<400>	44					
atgtctgacc	ctgtacgtat	tacaaatccc	ggtgcagaat	cgctggggta	tgattcagat	60
ggccatgaaa	ttatggccgt	tgatatTTtAT	gtaaaccctc	cacgtgtcga	tgtctttcat	120
ggtacccccg	ctgcatggag	ttccttcggg	aacaaaacca	tctggggcgg	aaacgagtg	180
gttgatgatt	ccccaacccg	aagtgatatc	gaaaaaaagg	acaaggaaat	cacagcgta	240
aaaaacacgc	tcagcgcgca	gcagaaagag	aatgagaata	agcgtactga	agccggaaaa	300
cgcctctctg	cggcgattgc	tcgaagggaa	aaagatgaaa	acacactgaa	aaactccgt	360
gccggaaaacg	cagatgccgc	tgatattaca	cgacaggagt	tcagactcct	gcaggcagag	420
ctgagagaaT	acggattccg	tactgaaatc	gccggatatg	acgccctccg	gctgcataca	480
gagagccgga	tgctgtttgc	tgatgctgat	tctcttcgta	tatctccccg	ggaggccagg	540
tcgttaatcg	aacaggctga	aaaacggcag	aaggatgCGc	agaacgcaga	caagaaggcc	600
gctgatatgc	ttgctgaata	cgagcgcaga	aaaggatttc	tggaaccccc	gttgtcagag	660
ctggaaaaaa	atggcggggc	agcccttgcc	gttcttgatg	cacaacaggc	ccgtctgctc	720
gggcagcaga	cacggaatga	cagggccatt	tcagaggccc	ggaataaact	cagttcagtg	780
acggaatcgc	ttaacacggc	ccgtaatgca	ttaaccagag	ctgaacaaca	cgtagcgcaa	840
cagaaaaaaca	cgcttgacgg	caaaacgata	gtttccctcg	aaaaattccc	ggggcgttca	900
tcaacaaatc	attctattgt	tgtgagcggt	gatccgagat	ttgccggtac	gataaaaaatc	960
acaaccagcg	cagtcatcga	taaccgtgca	aacctgaatt	atcttctgag	ccattccggt	1020
ctggactata	aacgcaatat	tctgaatgac	cggaatccgg	tggtgacaga	ggatgtggaa	1080
ggtgacaaga	aaatttataa	tgctgaagtt	gctgaatggg	ataagttacg	gcaaagattg	1140
cttgatgcca	gaaataaaat	cacctctgct	gaacttcggc	taaattccgc	gagaaataac	1200
ctcagtgcca	gaacaaatga	gcaaaagcat	gcaaatgacg	ctcttaatgc	cctgttgaag	1260
gaaaaaagaga	atatacgtaa	ccagctttcc	ggcatcaatc	agaagatagc	ggaagagaaa	1320
agaaaaacagg	atgaactgaa	ggcaacgaaa	gacgcaatta	atttcacaac	agagttcctg	1380
aaatcagttt	cagaaaaata	tggtgcaaaa	gctgagcagt	tagccagaga	gatggccggg	1440
caggctaaag	ggaagaaaat	acgtaatgtt	gaagaggcat	taaaaacgta	tgaaaagtac	1500
cgggctgaca	ttaacaaaaa	aattaatgca	aaagatcgTg	cagcgatttc	cgagccctt	1560
gagtcctgtg	agctgtctga	tatatcgtct	aatctgaaca	gattcagtcg	gggactggga	1620
tatgcaggaa	aatttacaag	tcttctgtag	tggtacactg	agtttggtaa	ggctgtccgg	1680
acagagaaact	ggcgtcctct	ttttgttaaa	acaqaaacca	tcatagcagg	caatgccgca	1740


```

acggctcttg tggcactggt cttcagtatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattgg gatcatacct aaatttggtg caccaaaacta catacagaag 1920
ttccagggca gatggtacca gcagctccca ggaacggccc ccaaactcct catctatagg 1980
aataatcagc ggccctca                                     1998

```

```

<210> 45
<211> 10
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> HBV HBsAg ScFv CDR1 from the heavy chain

```

```

<400> 45
Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser
 1             5             10

```

```

<210> 46
<211> 12
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> HBV HBsAg ScFv CDR3 from the light chain

```

```

<400> 46
Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser
 1             5             10

```

```

<210> 47
<211> 14
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> HBV HBsAg ScFv CDR1-CDR2 linker from the light
      chain

```

```

<400> 47
Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1             5             10

```

```

<210> 48
<211> 679
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> CDRs and FR from HBV HBsAg ScFv linked to Colicin
      Ia

```

```

<400> 48
Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu
 1             5             10             15
Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
 20             25             30

```

Tyr	Val	Ala	Ser	Asn	Pro	Pro	Arg	Val	Ala	Ser	Pro	Val	Phe	His	Gly	
	35						40					45				
Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	Gly	
	50					55					60					
Asn	Glu	Trp	Val	Ala	Ser	Pro	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	Glu	
65					70				75						80	
Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	
				85					90					95		
Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	
			100					105					110			
Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	
	115						120					125				
Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	
	130					135					140					
Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	
145					150					155					160	
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	
				165					170					175		
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	
			180					185					190			
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	
		195					200					205				
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	
	210					215					220					
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	
225					230					235					240	
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	
				245					250					255		
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	
		260						265					270			
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	
	275					280						285				
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	
	290					295					300					
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	
305					310					315					320	
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	
				325					330					335		
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	
			340				345					350				
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	
		355					360					365				
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	
	370					375					380					
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	
385					390					395					400	
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	
				405					410					415		
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	
			420					425					430			
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	
		435					440					445				
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	
	450					455					460					
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	
465					470					475					480	
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	
				485					490					495		
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	

	500		505		510
Tyr Arg Ala	Asp Ile Asn Lys Lys Ile Asn Ala Lys Asp Arg Ala Ala				
	515		520		525
Ile Ala Ala Ala	Leu Glu Ser Val Lys Leu Ser Asp Ile Ser Ser Asn				
	530		535		540
Leu Asn Arg Phe Ser Arg Gly Leu Gly Tyr Ala Gly Lys Phe Thr Ser					
545		550		555	560
Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Ala Arg Gly Thr					
	565		570		575
Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala Gly					
	580		585		590
Asn Ala Ala Thr Ala Leu Val Ala Leu Ala Leu Val Phe Ser Ile Leu					
	595		600		605
Thr Gly Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala Val					
	610		615		620
Thr Gly Ala Leu Ile Asp Glu Ser Leu Val Glu Lys Ala Asn Lys Phe					
625		630		635	640
Trp Gly Ile Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser Trp Ile Arg					
	645		650		655
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Asp Glu Ala Asp Tyr					
	660		665		670
Tyr Cys Asn Ser Arg Asp Ser					
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<210> 49

<211> 1986

<212> DNA

<213> Artificial sequence

<220>

<223> CDRs and FR from HBV HBsAg ScFv linked to Colicin

Ia

<400> 49

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ggtaccgccg ctgcatggag ttccttcggg aaaaaaacca tctggggcgg aaacgagtgg 180
gttgatgatt cccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtactga agccggaaaa 300
cgcctctctg cggcgattgc tgcaagggaa aaagatgaaa acacactgaa aacactccgt 360
gccggaaacg cagatgccgc tgatattaca cgacaggagt tcagactcct gcaggcagag 420
ctgagagaat acggattccg tactgaaatc gccggatatg acgccctccg gctgcataca 480
gagagccgga tgctgtttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540
tcgttaatcg aacaggctga aaaacggcag aaggatgcgc agaacgcaga caagaaggcc 600
gctgatatgc ttgctgaata cgagcgcaga aaaggtattc tggacaccgc gttgtcagag 660
ctggaaaaaa atggcggggc agcccttgcc gttcttgatg cacaacaggc ccgtctgctc 720
gggcagcaga cacggaatga cagggccatt tcagaggccc ggaataaaact cagttcagtg 780
acggaatcgc ttaacacggc ccgtaatgca ttaaccagag ctgaacaaca gctgacgcaa 840
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ggtgacaaga aaattttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
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ctcagtgcc gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcatcaatc agaagatagc ggaagagaaa 1320
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aaatcagttt cagaaaaata tgggtgcaaaa gctgagcagt tagccagaga gatggccggg 1440
caggctaaag ggaagaaaat acgtaatgtt gaagaggcat taaaaacgta tgaaaagtac 1500
cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgagccctt 1560

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gagtctgtga agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620
tatgcaggaa aatttacaag tcttgctgac tggatcactg agtttggttaa ggctgtccgg 1680
acagagaact ggcgtcctct ttttgttaaa acagaaacca tcatagcagg caatgccgca 1740
acggctcttg tggcactggg cttcagttatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccgggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattgg ctttaccttc agtgattatt atatgtcttg gattcgccag 1920
gcgccgggca aaggcctgga atgggtgtcc gatgaagcgg attattattg caacagccgc 1980
gattcc 1986

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<210> 50

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> G28 - S37 from HBV HBsAg ScFV

<400> 50

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Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser
1           5           10

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<210> 51

<211> 653

<212> PRT

<213> Artificial sequence

<220>

<223> G28 - S37 from HBV HBsAg ScFV linked to Colicin Ia

<400> 51

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Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu
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Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile
20           25           30
Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His Gly
35           40           45
Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly Gly
50           55           60
Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile Glu
65           70           75           80
Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala Gln
85           90           95
Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu Ser
100          105          110
Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr Leu
115          120          125
Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe Arg
130          135          140
Leu Leu Gln Ala Glu Leu Arg Glu Tyr Gly Phe Arg Thr Glu Ile Ala
145          150          155          160
Gly Tyr Asp Ala Leu Arg Leu His Thr Glu Ser Arg Met Leu Phe Ala
165          170          175
Asp Ala Asp Ser Leu Arg Ile Ser Pro Arg Glu Ala Arg Ser Leu Ile
180          185          190
Glu Gln Ala Glu Lys Arg Gln Lys Asp Ala Gln Asn Ala Asp Lys Lys
195          200          205
Ala Ala Asp Met Leu Ala Glu Tyr Glu Arg Arg Lys Gly Ile Leu Asp
210          215          220
Thr Arg Leu Ser Glu Leu Glu Lys Asn Gly Gly Ala Ala Leu Ala Val
225          230          235          240

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```

Leu Asp Ala Gln Gln Ala Arg Leu Leu Gly Gln Gln Thr Arg Asn Asp
                245                250                255
Arg Ala Ile Ser Glu Ala Arg Asn Lys Leu Ser Ser Val Thr Glu Ser
                260                265                270
Leu Asn Thr Ala Arg Asn Ala Leu Thr Arg Ala Glu Gln Gln Leu Thr
                275                280                285
Gln Gln Lys Asn Thr Pro Asp Gly Lys Thr Ile Val Ser Pro Glu Lys
                290                295                300
Phe Pro Gly Arg Ser Ser Thr Asn His Ser Ile Val Val Ser Gly Asp
305                310                315                320
Pro Arg Phe Ala Gly Thr Ile Lys Ile Thr Thr Ser Ala Val Ile Asp
                325                330                335
Asn Arg Ala Asn Leu Asn Tyr Leu Leu Ser His Ser Gly Leu Asp Tyr
                340                345                350
Lys Arg Asn Ile Leu Asn Asp Arg Asn Pro Val Val Thr Glu Asp Val
                355                360                365
Glu Gly Asp Lys Lys Ile Tyr Asn Ala Glu Val Ala Leu Ala Glu Trp
370                375                380
Asp Lys Leu Arg Gln Arg Leu Leu Asp Ala Arg Asn Lys Ile Thr Ser
385                390                395                400
Ala Glu Ser Ala Val Ala Ser Asn Ser Ala Arg Asn Asn Leu Ser Ala
                405                410                415
Arg Thr Asn Glu Gln Lys His Ala Asn Asp Ala Leu Asn Ala Leu Leu
                420                425                430
Lys Glu Lys Glu Asn Ile Arg Asn Gln Leu Ser Gly Ile Asn Gln Lys
435                440                445
Ile Ala Glu Glu Lys Arg Lys Gln Asp Glu Leu Lys Ala Thr Lys Asp
450                455                460
Ala Ile Asn Phe Thr Thr Glu Phe Leu Lys Ser Val Ser Glu Lys Tyr
465                470                475                480
Gly Ala Lys Ala Glu Gln Leu Ala Arg Glu Met Ala Gly Gln Ala Lys
                485                490                495
Gly Lys Lys Ile Arg Asn Val Glu Glu Ala Leu Lys Thr Tyr Glu Lys
500                505                510
Tyr Arg Ala Asp Ile Asn Lys Lys Ile Asn Ala Lys Asp Arg Ala Ala
515                520                525
Ile Ala Ala Ala Leu Glu Ser Val Lys Leu Ser Asp Ile Ser Ser Asn
530                535                540
Leu Asn Arg Phe Ser Arg Gly Leu Gly Tyr Ala Gly Lys Phe Thr Ser
545                550                555                560
Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Ala Arg Gly Thr
                565                570                575
Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala Gly
580                585                590
Asn Ala Ala Thr Ala Leu Val Ala Leu Ala Leu Val Phe Ser Ile Leu
595                600                605
Thr Gly Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala Val
610                615                620
Thr Gly Ala Leu Ile Asp Glu Ser Leu Val Glu Lys Ala Asn Lys Phe
625                630                635                640
Trp Gly Ile Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser
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<210> 52

<211> 1908

<212> DNA

<213> Artificial sequence

<220>

<223> G28 - S37 from HBV HBsAg ScFV linked to Colicin Ia

<400> 52

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ggtaccccg cgtcatggag ttccttcggg aacaaaacca tctggggcgg aaacgagtgg 180
gttgatgatt cccaacccg aagtgatatc gaaaaaaggg acaaggaaat cacagcgtac 240
aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtactga agccggaaaa 300
cgcctctctg cggcgattgc tgcaagggaa aaagatgaaa acacactgaa aacactccgt 360
gccggaaacg cagatgccgc tgatattaca cgacaggagt tcagactcct gcaggcagag 420
ctgagagaat acggattccg tactgaaatc gccggatatg acgccctccg gctgcataca 480
gagagccgga tgctgtttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540
tcgttaatcg aacaggctga aaaacggcag aaggatgcgc agaacgcaga caagaaggcc 600
gctgatatgc ttgctgaata cgagcgcaga aaaggtattc tggacaccgc gttgtcagag 660
ctggaaaaaa atggcggggc agcccttgcc gttcttgatg cacaacaggc ccgtctgctc 720
gggcagcaga cacggaatga cagggccatt tcagaggccc ggaataaact cagttcagtg 780
acggaatcgc ttaacacggc ccgtaatgca ttaaccagag ctgaacaaca gctgacgcaa 840
cagaaaaaca cgctgacgg caaaacgata gtttcccctg aaaaattccc ggggcgttca 900
tcaacaaatc attctattgt tgtgagcggg gatccgagat ttgccggtag gataaaaatc 960
acaaccagcg cagtcacgca taaccgtgca aacctgaatt atcttctgag ccattccggt 1020
ctggactata aacgcaatat tctgaatgac cggaatccgg tggtagacaga ggatgtggaa 1080
ggtgacaaga aaattttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
cttgatgcca gaaataaaat cacctctgct gaatctgcgg taaattcggc gagaaataac 1200
ctcagtgcca gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcataatc agaagatagc ggaagagaaa 1320
agaaaacagg atgaactgaa ggcaacgaaa gacgcaatta atttcacaac agagttcctg 1380
aatcagttt cagaaaaata tgggtgcaaaa gctgagcagt tagccagaga gatggccggg 1440
caggctaaag ggaagaaaat acgtaatgtt gaagaggcat taaaaacgta tgaaaagtac 1500
cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgcagccctt 1560
gagctgtgta agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620
tatgcaggaa aattttacaag tcttgctgac tggatcactg agtttggtaa ggctgtccgg 1680
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tatggtttac tgatggctgt caccggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtattgg attcaccttc agtgactact acatgagc 1908

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<210> 53

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> E217 - S228 from HBV HBsAg

<400> 53

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Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser
 1             5             10

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<210> 54

<211> 655

<212> PRT

<213> Artificial sequence

<220>

<223> E217 - S228 from HBV HBsAg ScFV linked to Colicin Ia

<400> 54

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Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu
 1             5             10             15

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			20					25					30		
Tyr	Val	Ala	Ser	Asn	Pro	Pro	Arg	Val	Ala	Ser	Pro	Val	Phe	His	Gly
		35					40					45			
Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	Gly
	50					55					60				
Asn	Glu	Trp	Val	Ala	Ser	Pro	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	Glu
65					70					75					80
Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln
			85						90					95	
Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser
			100					105					110		
Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu
		115					120					125			
Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg
	130					135					140				
Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala
145					150					155					160
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala
			165						170					175	
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile
			180					185					190		
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys
		195					200					205			
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp
	210					215					220				
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val
225					230					235					240
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp
			245						250					255	
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser
		260						265					270		
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr
		275					280					285			
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys
	290					295					300				
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp
305					310					315					320
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp
			325						330					335	
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr
			340					345					350		
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val
		355				360						365			
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp
	370					375					380				
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser
385					390					395					400
Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala
			405						410					415	
Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu
		420						425					430		
Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys
		435					440					445			
Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp
	450					455					460				
Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr
465					470					475					480
Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys
			485						490					495	
Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys

				500				505					510			
Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala	
		515					520					525				
Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn	
	530					535					540					
Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser	
545					550					555					560	
Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly	Thr	
				565					570					575		
Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala	Gly	
			580					585					590			
Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile	Leu	
		595					600					605				
Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala	Val	
	610					615					620					
Thr	Gly	Ala	Leu	Ile	Asp	Glu	Ser	Leu	Val	Glu	Lys	Ala	Asn	Lys	Phe	
625					630					635					640	
Trp	Gly	Ile	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser		
				645					650					655		

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<210> 55
<211> 1911
<212> DNA
<213> Artificial sequence
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<220>
<223> E217 - S228 from HBV HBsAg ScFv linked to Colicin
Ia

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cgctctctcg	cggcgattgc	tgcaaggga	aaagatgaaa	acacactgaa	aacactccgt	360	
gccggaaaacg	cagatgccgc	tgtatttaca	cgacaggagt	tcagactcct	gcaggcagag	420	
ctgagagaa	acggattccg	tactgaaatc	gccggatatg	acgccctccg	gctgcataca	480	
gagagccgga	tgctgtttgc	tgatgctgat	tctcttcgta	tatctccccg	ggaggccagg	540	
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ctggaaaaaa	atggcggggc	agcccttgcc	gttcttgatg	cacaacaggc	ccgtctgctc	720	
gggcagcaga	cacggaatga	cagggccatt	tcagaggccg	ggaataaact	cagttcagtg	780	
acggaatcgc	ttaaacaggc	cgtaatgca	ttaaccagag	ctgaacaaca	gctgacgcaa	840	
cagaaaaaca	cgctgacgg	caaaacgata	gtttccctg	aaaaattccc	ggggcgttca	900	
tcaacaatc	attctattgt	tgtgagcgg	gatccgagat	ttgccggtac	gataaaaaatc	960	
acaaccagcg	cagtcatcga	taaccgtgca	aacctgaatt	atcttctgag	ccattccggt	1020	
ctggactata	aacgcaatat	tctgaatgac	cggaatccgg	tggtgacaga	ggatgtggaa	1080	
ggtgacaaga	aaatttataa	tgctgaagtt	gctgaatggg	ataagttacg	gcaaagattg	1140	
cttgatgcca	gaaataaaa	cacctctgct	gaatctg	taaatccggc	gagaaataac	1200	
ctcagtgcca	gaacaaatga	gcaaaagcat	gcaaatgcag	ctcttaatgc	cctgttgaag	1260	
gaaaaagaga	ataacgtaa	ccagctttcc	ggcatcaatc	agaagatagc	ggaagagaaa	1320	
agaaaaacagg	atgaactgaa	ggcaacgaaa	gacgcaatta	atttcacaac	agagttcctg	1380	
aaatcagttt	cagaaaaata	tggtgcaaaa	gctgagcagt	tagccagaga	gatggccggg	1440	
caggctaaag	ggaagaaaat	acgtaatgtt	gaagaggcat	taaaaacgta	tgaaaagtac	1500	
cgggctgaca	ttaacaaaaa	aattaatgca	aaagatcgtg	cagcgattgc	cgcagccctt	1560	
gagtcgtgtga	agctgtctga	tatatcgtct	aatctgaaca	gattcagtcg	gggactggga	1620	
tatgcaggaa	aatttacaag	tcttctgtgac	tggatcactg	agttttggtaa	ggctgtccgg	1680	
acagagaact	ggcgctcctc	ttttgttaaa	acagaaacca	tcatagcagg	caatgccgca	1740	
acggctcttg	tggcactqgt	cttcagtatt	cttaccqgaa	qcqcttttaqg	cattatcqqg	1800	

tatgggtttac tgatggctgt caccgggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
 aataagttct ggggtattga tgaggctgac tattactgta actcccggga c 1911

<210> 56

<211> 650

<212> PRT

<213> Artificial sequence

<220>

<223> phage m13 peptide linked to colicin Ia

<400> 56

Met	Ser	Pro	Val	Ala	Arg	Gly	Ile	Thr	Asn	Pro	Gly	Ala	Glu	Ser	Leu	1	5	10	15
Gly	Tyr	Asp	Ser	Asp	Gly	His	Glu	Ile	Met	Ala	Val	Ala	Ser	Pro	Ile	20	25	30	
Tyr	Val	Ala	Ser	Asn	Pro	Pro	Arg	Val	Ala	Ser	Pro	Val	Phe	His	Gly	35	40	45	
Thr	Pro	Pro	Ala	Trp	Ser	Ser	Phe	Gly	Asn	Lys	Thr	Ile	Trp	Gly	Gly	50	55	60	
Asn	Glu	Trp	Val	Ala	Ser	Pro	Asp	Ser	Pro	Thr	Arg	Ser	Asp	Ile	Glu	65	70	75	80
Lys	Arg	Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	85	90	95	
Gln	Lys	Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	100	105	110	
Ala	Ala	Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	115	120	125	
Arg	Ala	Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	130	135	140	
Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	145	150	155	160
Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	165	170	175	
Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	180	185	190	
Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	195	200	205	
Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	210	215	220	
Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	225	230	235	240
Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	245	250	255	
Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	260	265	270	
Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	275	280	285	
Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	290	295	300	
Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	305	310	315	320
Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	325	330	335	
Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	340	345	350	
Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	355	360	365	
Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	370	375	380	
Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser				

```

385          390          395          400
Ala Glu Ser Ala Val Ala Ser Asn Ser Ala Arg Asn Asn Leu Ser Ala
          405          410          415
Arg Thr Asn Glu Gln Lys His Ala Asn Asp Ala Leu Asn Ala Leu Leu
          420          425          430
Lys Glu Lys Glu Asn Ile Arg Asn Gln Leu Ser Gly Ile Asn Gln Lys
          435          440          445
Ile Ala Glu Glu Lys Arg Lys Gln Asp Glu Leu Lys Ala Thr Lys Asp
          450          455          460
Ala Ile Asn Phe Thr Thr Glu Phe Leu Lys Ser Val Ser Glu Lys Tyr
465          470          475          480
Gly Ala Lys Ala Glu Gln Leu Ala Arg Glu Met Ala Gly Gln Ala Lys
          485          490          495
Gly Lys Lys Ile Arg Asn Val Glu Glu Ala Leu Lys Thr Tyr Glu Lys
          500          505          510
Tyr Arg Ala Asp Ile Asn Lys Lys Ile Asn Ala Lys Asp Arg Ala Ala
          515          520          525
Ile Ala Ala Ala Leu Glu Ser Val Lys Leu Ser Asp Ile Ser Ser Asn
          530          535          540
Leu Asn Arg Phe Ser Arg Gly Leu Gly Tyr Ala Gly Lys Phe Thr Ser
545          550          555          560
Leu Ala Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Ala Arg Gly Thr
          565          570          575
Glu Asn Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala Gly
          580          585          590
Asn Ala Ala Thr Ala Leu Val Ala Leu Ala Leu Val Phe Ser Ile Leu
          595          600          605
Thr Gly Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala Val
          610          615          620
Thr Gly Ala Leu Ile Asp Glu Ser Leu Val Glu Lys Ala Asn Lys Phe
625          630          635          640
Trp Gly Ile Thr Leu Thr Thr Lys Leu Tyr
          645          650

```

<210> 57

<211> 653

<212> PRT

<213> Artificial sequence

<220>

<223> phage m13 peptide linked to colicin Ia

<400> 57

```

Met Ser Asp Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser
 1          5          10          15
Leu Gly Tyr Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro
          20          25          30
Ile Tyr Val Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His
          35          40          45
Gly Thr Pro Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly
          50          55          60
Gly Asn Glu Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile
65          70          75          80
Glu Lys Arg Asp Lys Glu Ile Thr Ala Tyr Lys Asn Thr Leu Ser Ala
          85          90          95
Gln Gln Lys Glu Asn Glu Asn Lys Arg Thr Glu Ala Gly Lys Arg Leu
          100          105          110
Ser Ala Ala Ile Ala Ala Arg Glu Lys Asp Glu Asn Thr Leu Lys Thr
          115          120          125
Leu Arg Ala Gly Asn Ala Asp Ala Ala Asp Ile Thr Arg Gln Glu Phe

```

130		135		140											
Arg	Leu	Leu	Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile
145					150					155					160
Ala	Gly	Tyr	Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe
				165						170					175
Ala	Asp	Ala	Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu
				180						185				190	
Ile	Glu	Gln	Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys
				195						200				205	
Lys	Ala	Ala	Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu
				210						215				220	
Asp	Thr	Arg	Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala
225					230					235					240
Val	Leu	Asp	Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn
				245						250					255
Asp	Arg	Ala	Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu
				260						265					270
Ser	Leu	Asn	Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu
				275						280					285
Thr	Gln	Gln	Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu
				290						295					300
Lys	Phe	Pro	Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly
305					310					315					320
Asp	Pro	Arg	Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile
				325						330					335
Asp	Asn	Arg	Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp
				340						345					350
Tyr	Lys	Arg	Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp
				355						360					365
Val	Glu	Gly	Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu
				370						375					380
Trp	Asp	Lys	Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr
385					390					395					400
Ser	Ala	Glu	Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser
				405						410					415
Ala	Arg	Thr	Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu
				420						425					430
Leu	Lys	Glu	Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln
				435						440					445
Lys	Ile	Ala	Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys
				450						455					460
Asp	Ala	Ile	Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys
465					470					475					480
Tyr	Gly	Ala	Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala
				485						490					495
Lys	Gly	Lys	Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu
				500						505					510
Lys	Tyr	Arg	Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala
				515						520					525
Ala	Ile	Ala	Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser
				530						535					540
Asn	Leu	Asn	Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr
545					550					555					560
Ser	Leu	Ala	Asp	Trp	Ile	Thr	Glu	Phe	Gly	Lys	Ala	Val	Ala	Arg	Gly
				565						570					575
Thr	Glu	Asn	Trp	Arg	Pro	Leu	Phe	Val	Lys	Thr	Glu	Thr	Ile	Ile	Ala
				580						585					590
Gly	Asn	Ala	Ala	Thr	Ala	Leu	Val	Ala	Leu	Ala	Leu	Val	Phe	Ser	Ile
				595						600					605
Leu	Thr	Gly	Ser	Ala	Leu	Gly	Ile	Ile	Gly	Tyr	Gly	Leu	Leu	Met	Ala
610															620

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<220>
<223> phage m13 peptide linked to colicin Ia
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<210> 59
<211> 1904
<212> DNA
<213> Artificial sequence
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<400> 59						
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ggccatgaaa	ttagtggccg	tgatatttat	gtaaacacctc	cacgtgtcga	tgtctttcat	120
ggtaccccg	ctgcattggag	tctcttcggg	aacaaaaacca	tctggggcgg	aaacgagtg	180
gttgatgatt	ccccaacccq	aagtqatatc	qaaaaaaqqq	acaaqqaat	cacacgctac	240

```

aaaaacacgc tcagcgcgca gcagaaagag aatgagaata agcgtactga agccggaaaa 300
cgctctctcg cggcgattgc tgcaagggaa aaagatgaaa acacactgaa aacactccgt 360
gccggaaaacg cagatgccgc tgatattaca cgacaggagt tcagactcct gcaggcagag 420
ctgagagaaat acggattccg tactgaaatc gccggatatg acgccctccg gctgcataca 480
gagagccgga tgctgtttgc tgatgctgat tctcttcgta tatctccccg ggaggccagg 540
tcgttaatcg aacaggctga aaaacggcag aaggatgcgc agaacgcaga caagaaggcc 600
gctgatatgc ttgctgaata cgagcgcaga aaaggatttc tggacacccg gttgtcagag 660
ctggaaaaaaa atggcggggc agcccttgcc gttcttgatg cacaacaggc ccgtctgctc 720
gggcagcaga cacggaatga cagggccatt tcagaggccc ggaataaaact cagttcagtg 780
acggaatcgc ttaacacggc ccgtaatgca ttaaccagag ctgaacaaca gctgacgcaa 840
cagaaaaaca cgcctgacgg caaaacgata gtttccccctg aaaaattccc ggggcgttca 900
tcaacaaatc attctattgt tgtgagcggg gatccgagat ttgccggtag gataaaaaatc 960
acaaccagcg cagtcatcga taaccgtgca aacctgaatt atcttctgag ccattccggt 1020
ctggactata aacgcaatat tctgaatgac cgggaatccgg tggtgacaga ggatgtggaa 1080
ggtgacaaga aaatttataa tgctgaagtt gctgaatggg ataagttacg gcaaagattg 1140
cttgatgccg gaaataaaaat cacctctgct gaatctgcgg taaattcggc gagaaataac 1200
ctcagtgccg gaacaaatga gcaaaagcat gcaaatgacg ctcttaatgc cctgttgaag 1260
gaaaaagaga atatacgtaa ccagctttcc ggcataatc agaagatagc ggaagagaaa 1320
agaaaacagg atgaactgaa ggcaacgaaa gacgcaatta atttcacaac agagttcctg 1380
aaatcagttt cagaaaaata tgggtgcaaaa gctgagcagt tagccagaga gatggccggg 1440
caggctaaag ggaagaaaat acgtaatggt gaagaggcat taaaaacgta tgaaaagtac 1500
cgggctgaca ttaacaaaaa aattaatgca aaagatcgtg cagcgattgc cgcagccctt 1560
gagtctgtga agctgtctga tatatcgtct aatctgaaca gattcagtcg gggactggga 1620
tatgcaggaa aattttacaag tcttgctgac tggatcactg agtttggtta ggctgtccgg 1680
acagagaact ggcgtcctct ttttggttaa acagaaacca tcatagcagg caatgccgca 1740
acggctcttg tggcactggt cttcagtatt cttaccggaa gcgctttagg cattatcggg 1800
tatggtttac tgatggctgt caccggtgcg ctgattgatg aatcgcttgt ggaaaaagcg 1860
aataagttct ggggtatttg tactctcact accaactata ctgt 1904

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<210> 60

<211> 13

<212> PRT

<213> Candida albicans

<400> 60

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Gly Phe Arg Leu Thr Asn Phe Gly Tyr Phe Glu Pro Gly
 1             5             10

```

<210> 61

<211> 657

<212> PRT

<213> Artificial sequence

<220>

<223> Candida albicans alpha mating pheromone attached
to colicin

<400> 61

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Gly Phe Arg Leu Thr Asn Phe Gly Tyr Phe Glu Pro Gly Met Ser Asp
 1             5             10             15
Pro Val Ala Arg Gly Ile Thr Asn Pro Gly Ala Glu Ser Leu Gly Tyr
          20          25          30
Asp Ser Asp Gly His Glu Ile Met Ala Val Ala Ser Pro Ile Tyr Val
          35          40          45
Ala Ser Asn Pro Pro Arg Val Ala Ser Pro Val Phe His Gly Thr Pro
          50          55          60
Pro Ala Trp Ser Ser Phe Gly Asn Lys Thr Ile Trp Gly Gly Asn Glu
65          70          75          80
Trp Val Ala Ser Pro Asp Ser Pro Thr Arg Ser Asp Ile Glu Lys Arg

```

85					90					95					
Asp	Lys	Glu	Ile	Thr	Ala	Tyr	Lys	Asn	Thr	Leu	Ser	Ala	Gln	Gln	Lys
			100					105					110		
Glu	Asn	Glu	Asn	Lys	Arg	Thr	Glu	Ala	Gly	Lys	Arg	Leu	Ser	Ala	Ala
			115					120					125		
Ile	Ala	Ala	Arg	Glu	Lys	Asp	Glu	Asn	Thr	Leu	Lys	Thr	Leu	Arg	Ala
			130					135					140		
Gly	Asn	Ala	Asp	Ala	Ala	Asp	Ile	Thr	Arg	Gln	Glu	Phe	Arg	Leu	Leu
			145					150					155		
Gln	Ala	Glu	Leu	Arg	Glu	Tyr	Gly	Phe	Arg	Thr	Glu	Ile	Ala	Gly	Tyr
				165					170					175	
Asp	Ala	Leu	Arg	Leu	His	Thr	Glu	Ser	Arg	Met	Leu	Phe	Ala	Asp	Ala
			180					185					190		
Asp	Ser	Leu	Arg	Ile	Ser	Pro	Arg	Glu	Ala	Arg	Ser	Leu	Ile	Glu	Gln
			195					200					205		
Ala	Glu	Lys	Arg	Gln	Lys	Asp	Ala	Gln	Asn	Ala	Asp	Lys	Lys	Ala	Ala
			210					215					220		
Asp	Met	Leu	Ala	Glu	Tyr	Glu	Arg	Arg	Lys	Gly	Ile	Leu	Asp	Thr	Arg
			225					230					235		
Leu	Ser	Glu	Leu	Glu	Lys	Asn	Gly	Gly	Ala	Ala	Leu	Ala	Val	Leu	Asp
				245					250				255		
Ala	Gln	Gln	Ala	Arg	Leu	Leu	Gly	Gln	Gln	Thr	Arg	Asn	Asp	Arg	Ala
			260					265					270		
Ile	Ser	Glu	Ala	Arg	Asn	Lys	Leu	Ser	Ser	Val	Thr	Glu	Ser	Leu	Asn
			275					280					285		
Thr	Ala	Arg	Asn	Ala	Leu	Thr	Arg	Ala	Glu	Gln	Gln	Leu	Thr	Gln	Gln
			290					295					300		
Lys	Asn	Thr	Pro	Asp	Gly	Lys	Thr	Ile	Val	Ser	Pro	Glu	Lys	Phe	Pro
			305					310					315		
Gly	Arg	Ser	Ser	Thr	Asn	His	Ser	Ile	Val	Val	Ser	Gly	Asp	Pro	Arg
				325					330				335		
Phe	Ala	Gly	Thr	Ile	Lys	Ile	Thr	Thr	Ser	Ala	Val	Ile	Asp	Asn	Arg
			340					345					350		
Ala	Asn	Leu	Asn	Tyr	Leu	Leu	Ser	His	Ser	Gly	Leu	Asp	Tyr	Lys	Arg
			355					360					365		
Asn	Ile	Leu	Asn	Asp	Arg	Asn	Pro	Val	Val	Thr	Glu	Asp	Val	Glu	Gly
			370					375					380		
Asp	Lys	Lys	Ile	Tyr	Asn	Ala	Glu	Val	Ala	Leu	Ala	Glu	Trp	Asp	Lys
			385					390					395		
Leu	Arg	Gln	Arg	Leu	Leu	Asp	Ala	Arg	Asn	Lys	Ile	Thr	Ser	Ala	Glu
				405					410				415		
Ser	Ala	Val	Ala	Ser	Asn	Ser	Ala	Arg	Asn	Asn	Leu	Ser	Ala	Arg	Thr
			420					425					430		
Asn	Glu	Gln	Lys	His	Ala	Asn	Asp	Ala	Leu	Asn	Ala	Leu	Leu	Lys	Glu
			435					440					445		
Lys	Glu	Asn	Ile	Arg	Asn	Gln	Leu	Ser	Gly	Ile	Asn	Gln	Lys	Ile	Ala
			450					455					460		
Glu	Glu	Lys	Arg	Lys	Gln	Asp	Glu	Leu	Lys	Ala	Thr	Lys	Asp	Ala	Ile
			465					470					475		
Asn	Phe	Thr	Thr	Glu	Phe	Leu	Lys	Ser	Val	Ser	Glu	Lys	Tyr	Gly	Ala
				485					490				495		
Lys	Ala	Glu	Gln	Leu	Ala	Arg	Glu	Met	Ala	Gly	Gln	Ala	Lys	Gly	Lys
			500					505					510		
Lys	Ile	Arg	Asn	Val	Glu	Glu	Ala	Leu	Lys	Thr	Tyr	Glu	Lys	Tyr	Arg
			515					520					525		
Ala	Asp	Ile	Asn	Lys	Lys	Ile	Asn	Ala	Lys	Asp	Arg	Ala	Ala	Ile	Ala
			530					535					540		
Ala	Ala	Leu	Glu	Ser	Val	Lys	Leu	Ser	Asp	Ile	Ser	Ser	Asn	Leu	Asn
			545					550					555		
Arg	Phe	Ser	Arg	Gly	Leu	Gly	Tyr	Ala	Gly	Lys	Phe	Thr	Ser	Leu	Ala
				565					570					575	

Asp Trp Ile Thr Glu Phe Gly Lys Ala Val Ala Arg Gly Thr Glu Asn
 580 585 590
 Trp Arg Pro Leu Phe Val Lys Thr Glu Thr Ile Ile Ala Gly Asn Ala
 595 600 605
 Ala Thr Ala Leu Val Ala Leu Ala Leu Val Phe Ser Ile Leu Thr Gly
 610 615 620
 Ser Ala Leu Gly Ile Ile Gly Tyr Gly Leu Leu Met Ala Val Thr Gly
 625 630 635 640
 Ala Leu Ile Asp Glu Ser Leu Val Glu Lys Ala Asn Lys Phe Trp Gly
 645 650 655
 Ile

<210> 62

<211> 1917

<212> DNA

<213> Artificial sequence

<220>

<223> Candida albicans alpha mating pheromone attached
to colicin

<400> 62

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acaaatcccg gtgcagaatc gctgggggtat gattcagatg gccatgaaat tatggccggt 120
gatatttatg taaacccctcc acgtgtcgcg gtctttcatg gtaccccgcc tgcatggagt 180
tccttcggga acaaaacccat ctggggcgga aacgagtggg ttgatgattc cccaaccgca 240
agtgatatcg aaaaaaggga caaggaaatc acagcgtaca aaaacacgct cagcgcgag 300
cagaaagaga atgagaataa gcgtactgaa gccggaaaac gcctctctgc ggcgattgct 360
gcaagggaaa aagatgaaaa cactactgaa acactccgtg ccggaaaacgc agatgccgct 420
gatattacac gacaggagtt cagactcctg caggcagagc tgagagaata cggattccgt 480
actgaaatcg ccggatatga cgccctccgg ctgcatacag agagccggat gctgtttgct 540
gatgctgatt ctcttcgtat atctccccgg gaggccaggt cgtaaatcga acaggctgaa 600
aaacggcaga aggatgcgca gaacgcagac aagaaggccg ctgatatgct tgctgaatac 660
gagcgagaaa aaggtattct ggacacccgg ttgtcagagc tggaaaaaaa tggcggggca 720
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